

Exhibit A



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Sazani et al.(10) **Pub. No.: US 2010/0130591 A1**
(43) **Pub. Date:** **May 27, 2010**(54) **MULTIPLE EXON SKIPPING
COMPOSITIONS FOR DMD**(76) Inventors: **Peter Sazani**, Bothell, WA (US);
Ryszard Kole, Bellevue, WA (US)Correspondence Address:
**SEED INTELLECTUAL PROPERTY LAW
GROUP PLLC**
701 FIFTH AVE, SUITE 5400
SEATTLE, WA 98104 (US)(21) Appl. No.: **12/605,276**(22) Filed: **Oct. 23, 2009****Related U.S. Application Data**(60) Provisional application No. 61/108,416, filed on Oct.
24, 2008.**Publication Classification**(51) **Int. Cl.***A61K 31/7088* (2006.01)
C07H 21/02 (2006.01)
C07K 9/00 (2006.01)
A61P 21/00 (2006.01)(52) **U.S. Cl.** **514/44 A; 536/24.5; 530/322**

(57)

ABSTRACT

Provided are antisense molecules capable of binding to a selected target site in the human dystrophin gene to induce exon skipping, and methods of use thereof to treat muscular dystrophy.

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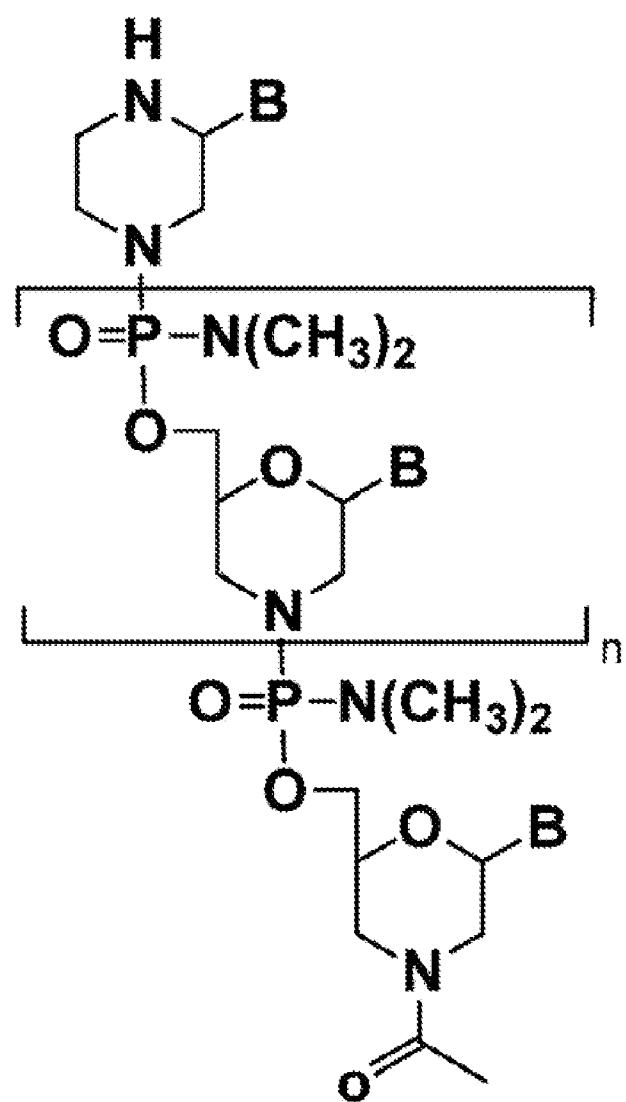


FIG. 1A

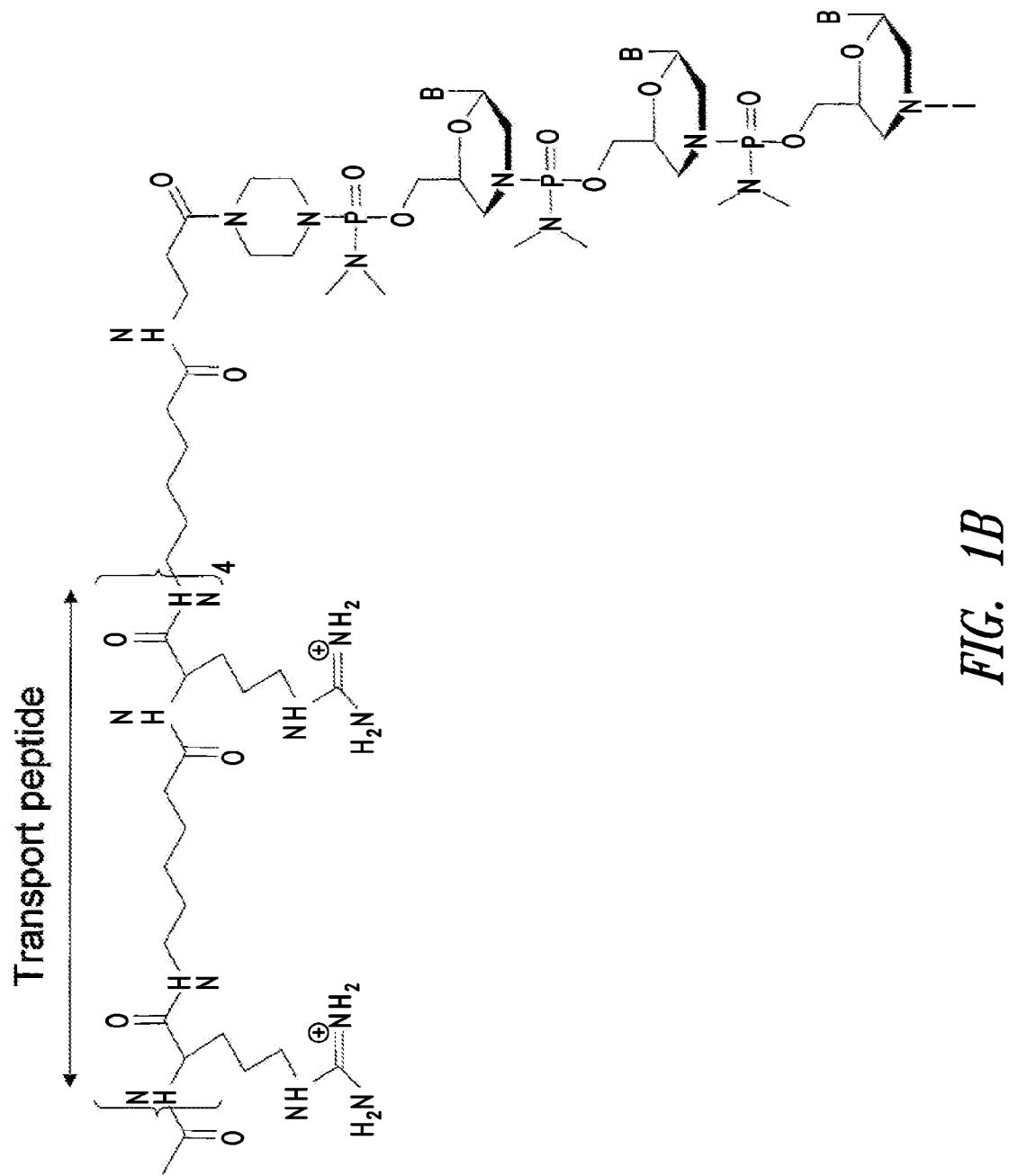


FIG. 1B

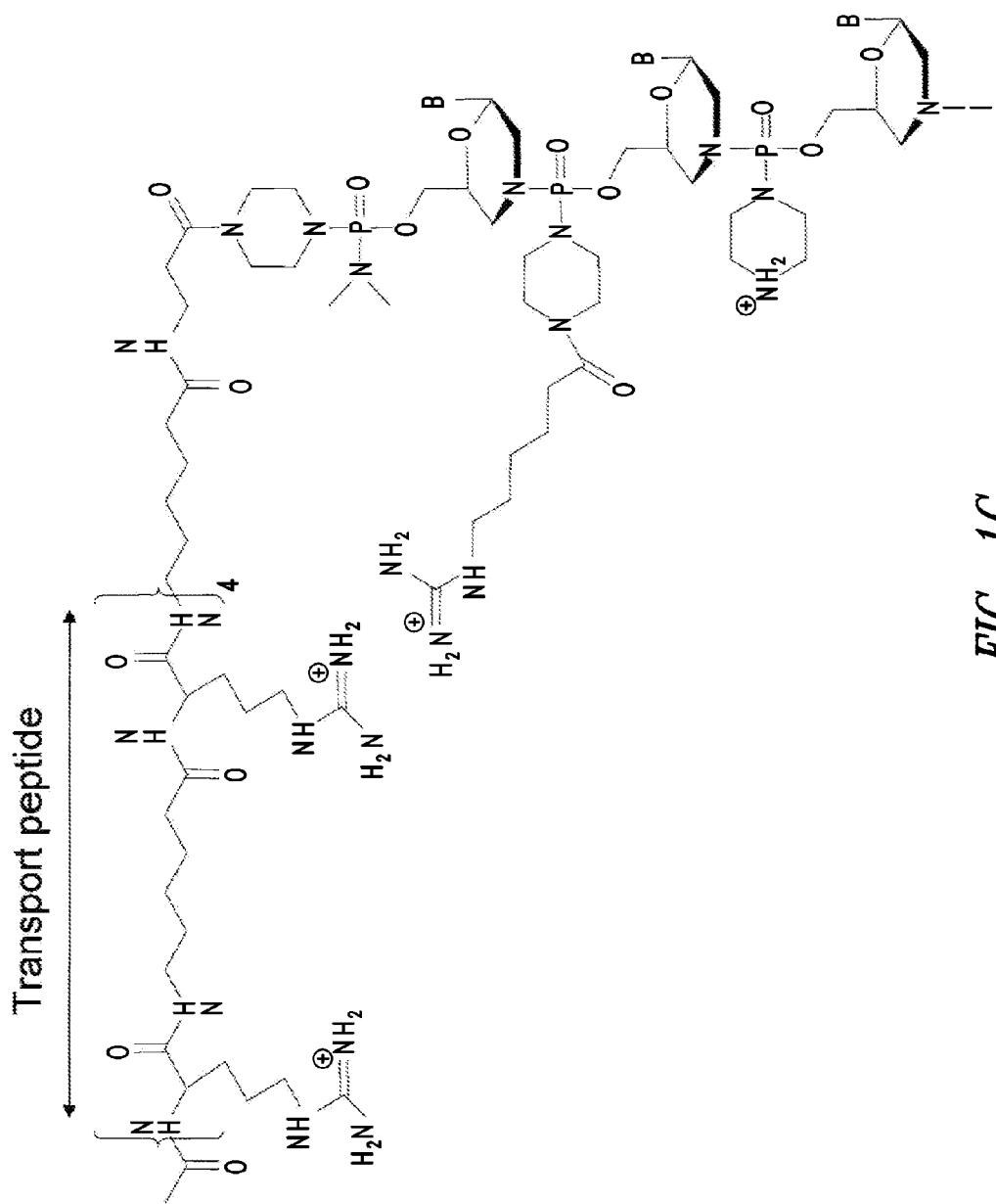


FIG. 1C

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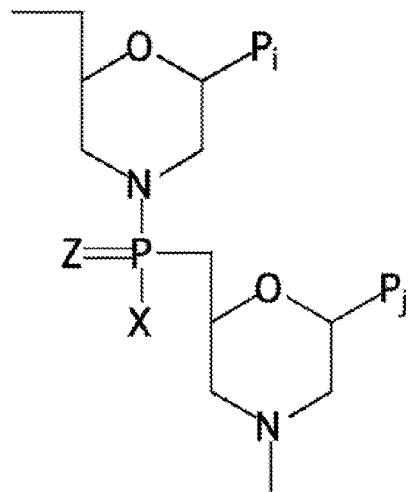


FIG. 1D

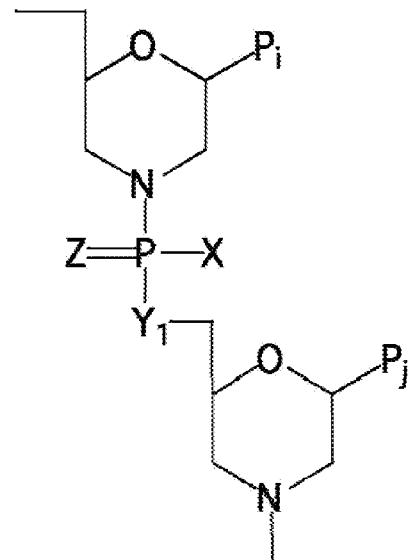


FIG. 1E

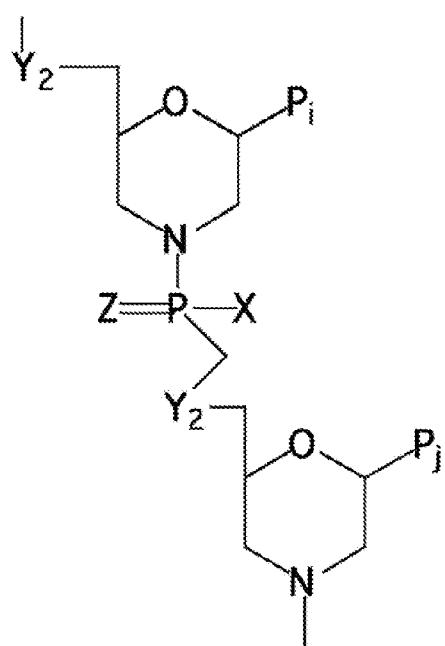


FIG. 1F

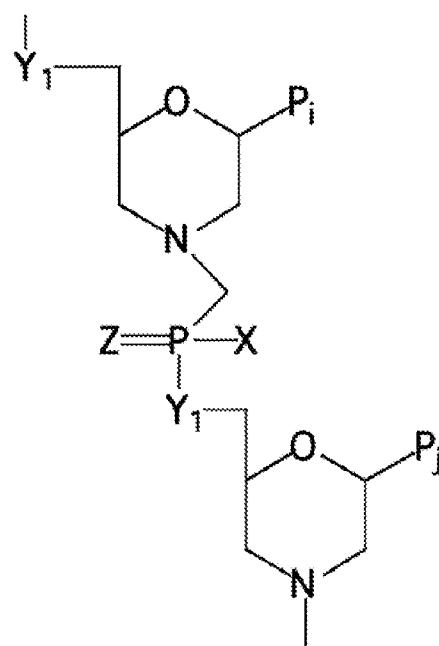
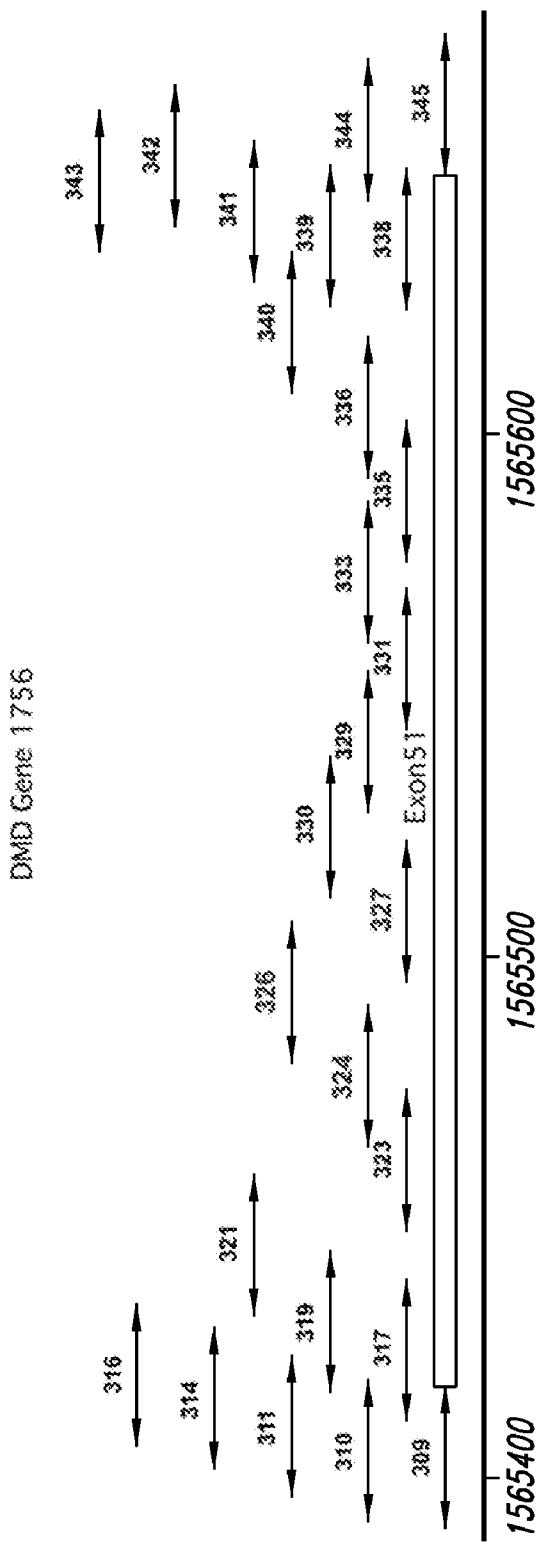


FIG. 1G

Dystrophin Exon 51 Scan Oligos



Oligo SEQ ID NOS shown – SEQ ID NOS 324, 326 and 327 were most effective

FIG. 2A

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Exon 51S.3 (RD)

High-Purity Synthesis, 3.0uM, RD Cells

FIG. 2B

51MCS (Muscle Cell Competitor Screen)

High-Purity Synthesis, 3.0uM, Human Primary Skeletal Muscle Cells

Oligo	Name; SEQ ID NO	Lot
NG-07-1160	AVI-5658; 588	09MY11-R(E4)
NG-09-0053	053; 324	09JNJ12-R(A4)
NG-09-0054	054; 326	09JNJ12-R(B4)
NG-09-0055	055; 327	09JNJ12-R(E4)
NG-08-0835	h51AON1; 594	09JL07-R(A1)

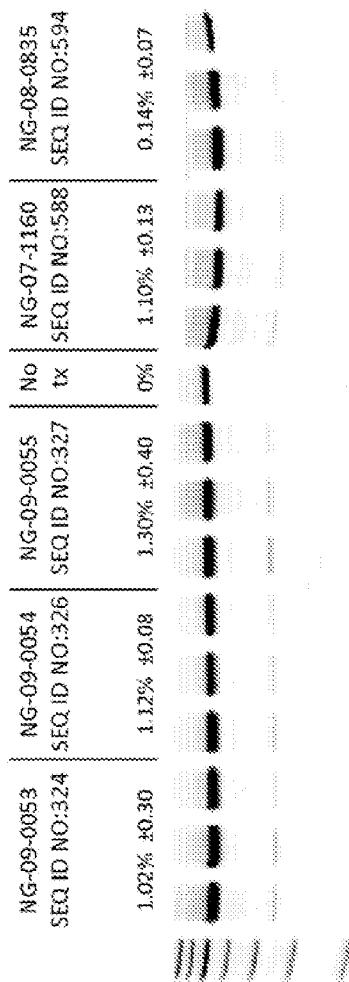


FIG. 2C

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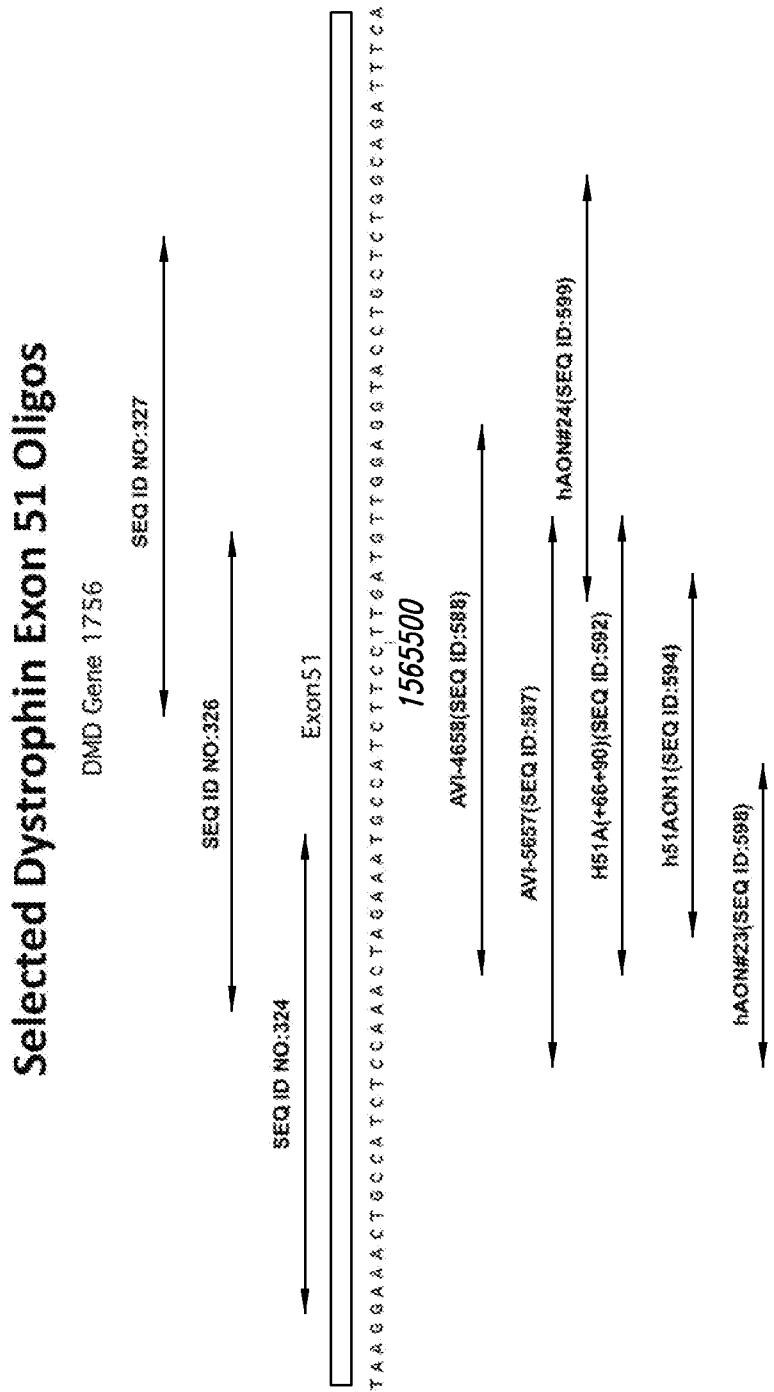


FIG. 2D

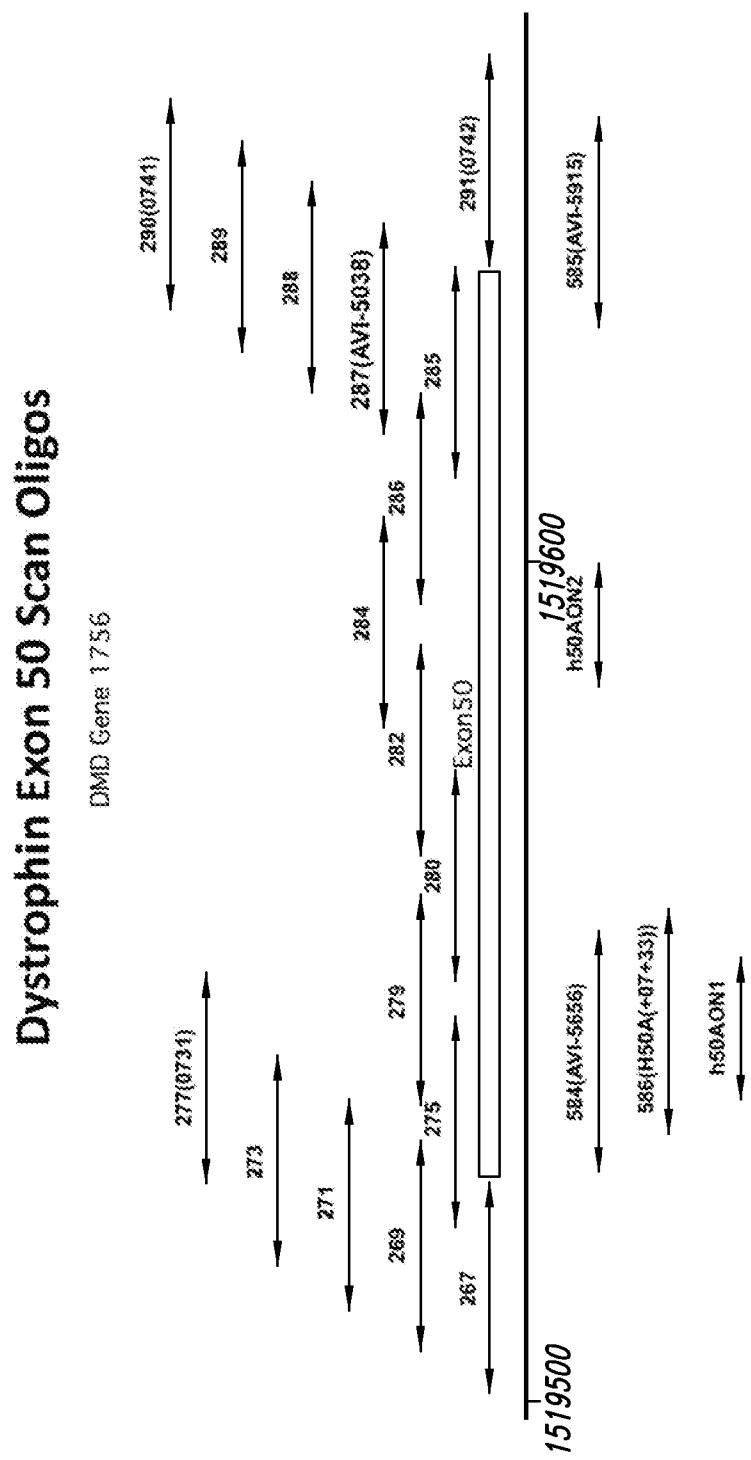
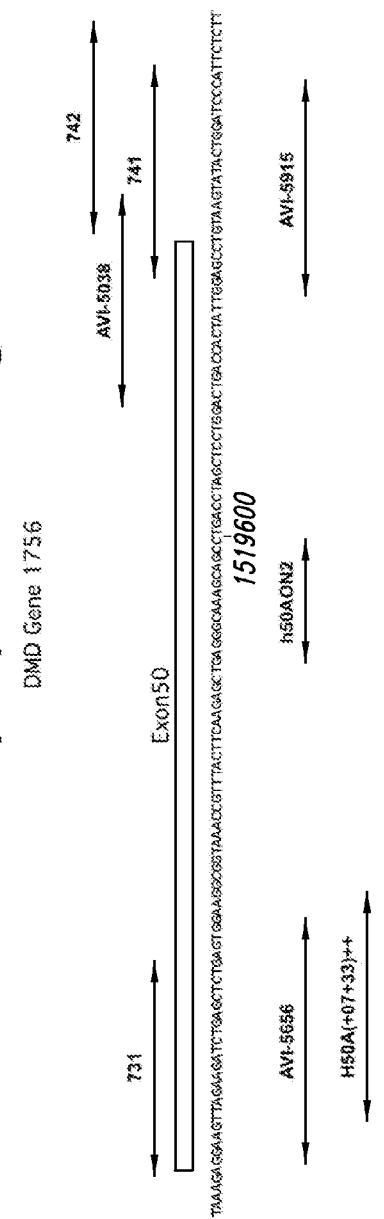


FIG. 3A

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Selected Dystrophin Exon 50 Oligos



Compound	EC_{50} (micromolar)*
AVI-5656 (SEQ ID NO:584)	0.921
AVI-5915 (SEQ ID NO:585)	3.693
NG-08-0731 (SEQ ID NO:277)	1.741
AVI-5038 (SEQ ID NO:287)	0.966
NG-08-0741 (SEQ ID NO:290)	1.836
NG-08-0742 (SEQ ID NO:291)	2.402

* Determined from dose-ranging studies in RD cells
AVI #00453 - 02FEB2009

FIG. 3B

Dystrophin Exon 53 Scan Oligos

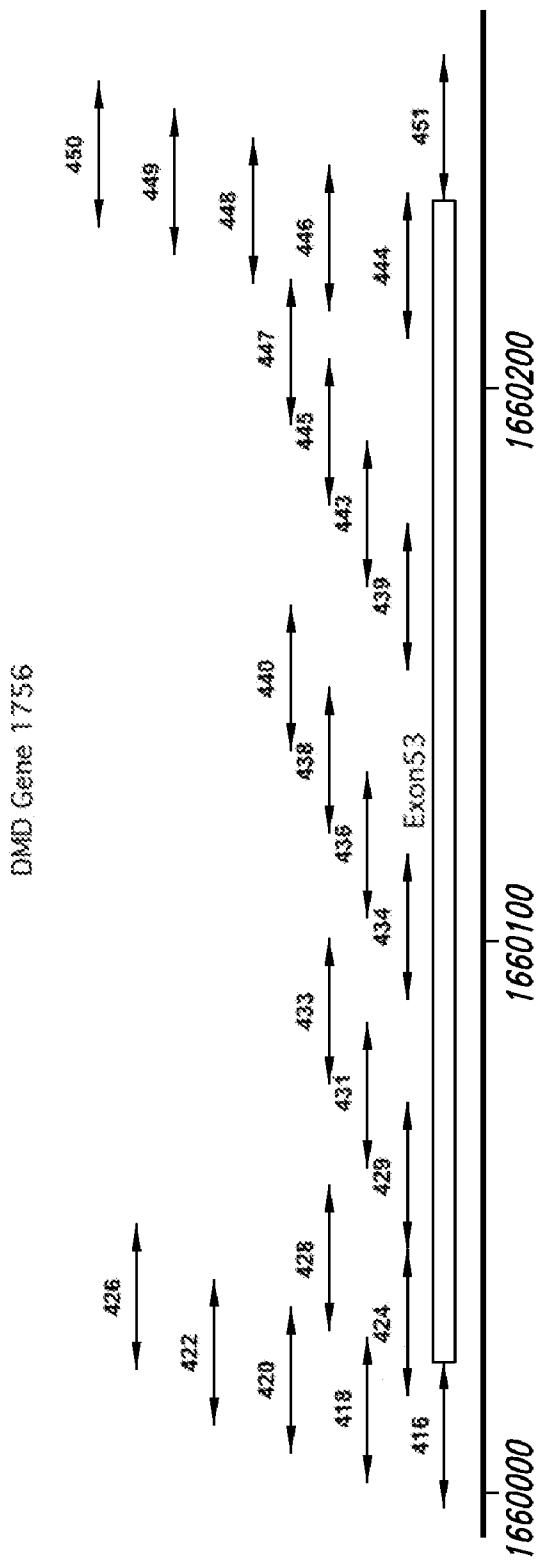


FIG. 4A

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Selected Dystrophin Exon 53 Oligos

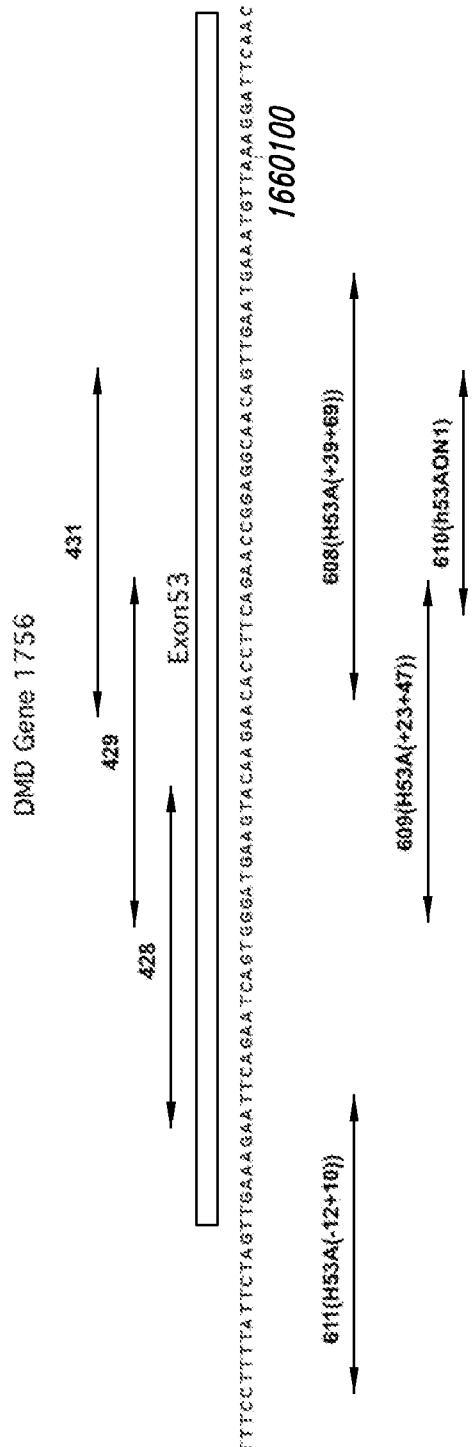


FIG. 4B

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Exon 53 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0uM) RD Cells

NG-0746 09AU11-R(E5) (SEQ ID NO: 422)



FIG. 4C

ExOn 53 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0 μ M) RD Cells

NG-0749 09AU11-R(A7) (SEQ ID NO: 428)

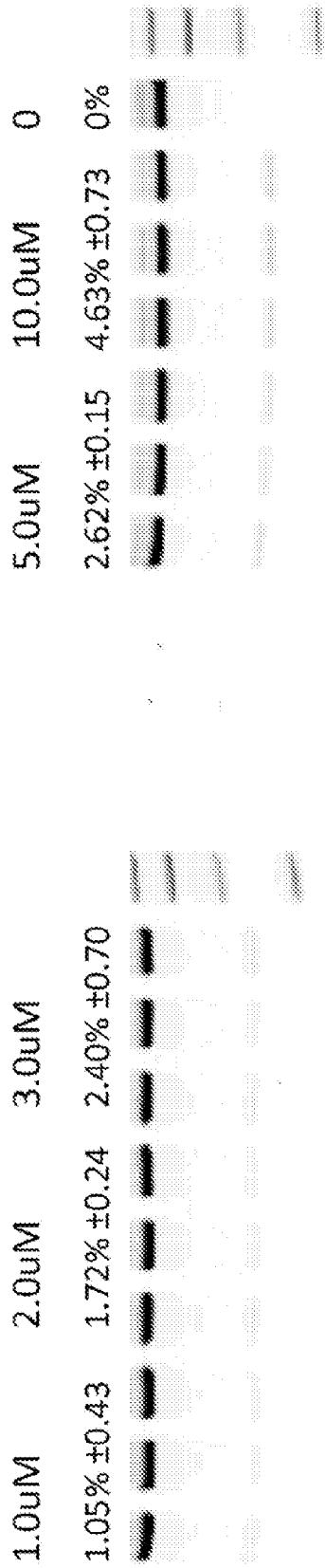


FIG. 4D

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Exon 53 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0uM) RD Cells

NG-0750 09AU11-R(C7) (SEQ ID NO: 429)

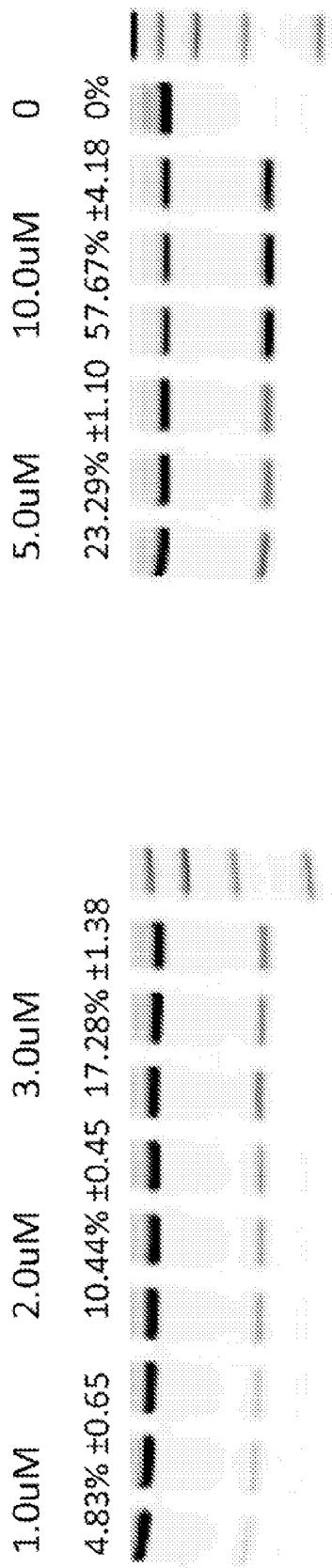


FIG. 4E

ExOn 53 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0uM) RD Cells

NG-0751 09AU11-J(E7) (SEQ ID NO: 431)

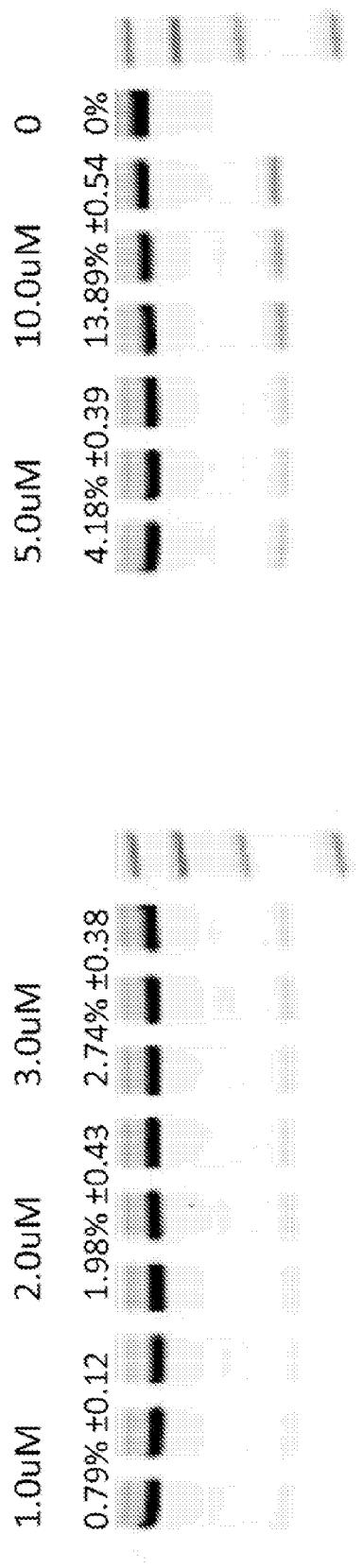


FIG. 4F

Exon53 RD Cell Dose-Range Summary

	Percent Exon Skipped		
Treatment (uM)	746 (SEQ ID N0:422)	749 (SEQ ID N0:428)	750 (SEQ ID N0:429)
1.0	0.00	1.05	4.83
2.0	0.00	1.72	10.44
3.0	0.00	2.40	17.28
5.0	0.54	2.62	23.29
10	3.53	4.63	57.67
EC ₅₀ (uM)	NA	72.2	9.3
			25.3

FIG. 4G

Exon 53 CS (Competitor Screen)

High-Purity Synthesis, 3.0uM, RD Cells

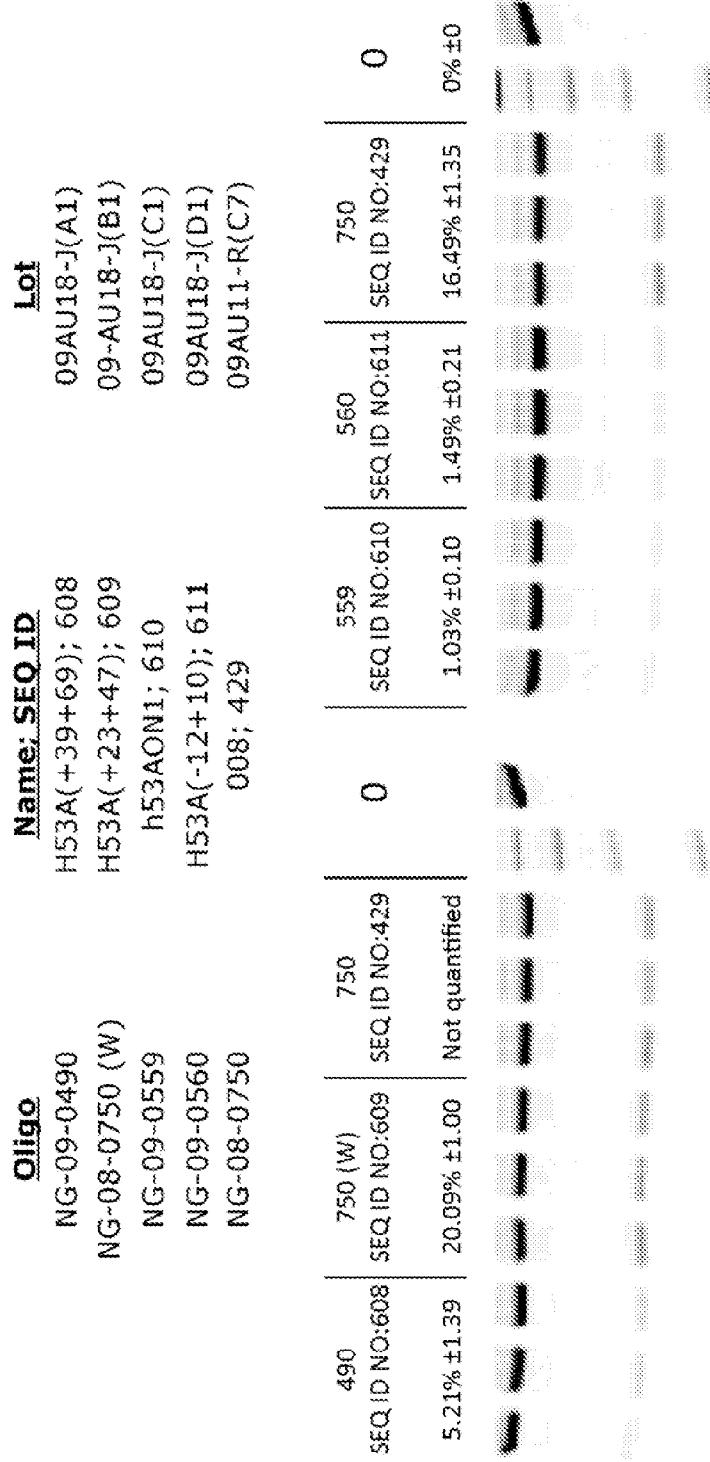


FIG. 4H

Exon 53 MCS (Muscle Cell Competitor Screen)

High-Purity Synthesis, 3.0uM, Human Primary Skeletal Muscle Cells

<u>Oligo</u>	<u>Name: SEQ ID</u>	<u>Lot</u>
NG-09-0490	H53A(+39+69); 608	09AU18-J(A1)
NG-08-0750 (W)	H53A(+23+47); 609	09-AU18-J(B1)
NG-09-0559	h53AON1; 610	09AU18-J(C1)
NG-09-0560	H53A(-12+10); 611	09AU18-J(D1)
NG-08-0750	008; 429	09AU11-R(C7)

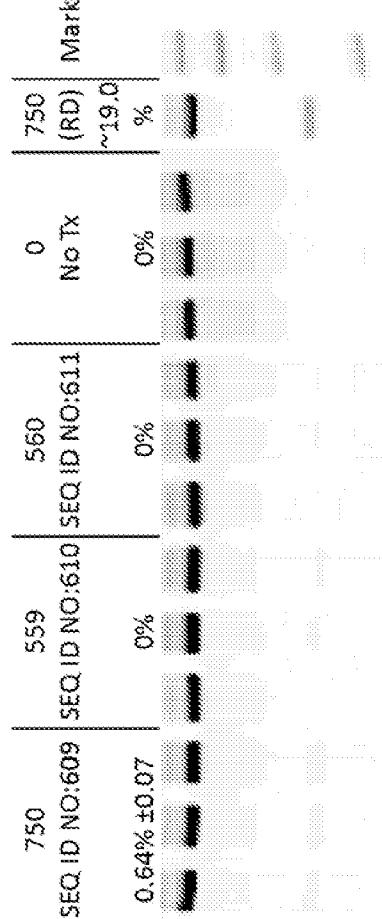


FIG. 4I

Dystrophin Exon 44 Scan Oligos

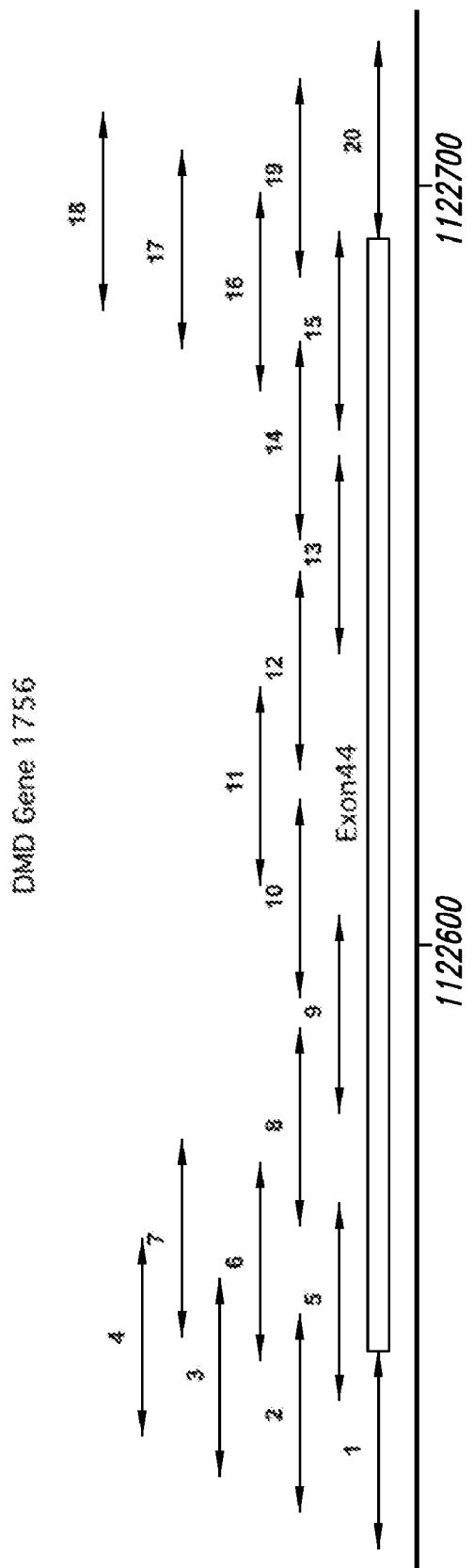


FIG. 5A

Selected Dystrophin Exon 44 Oligos

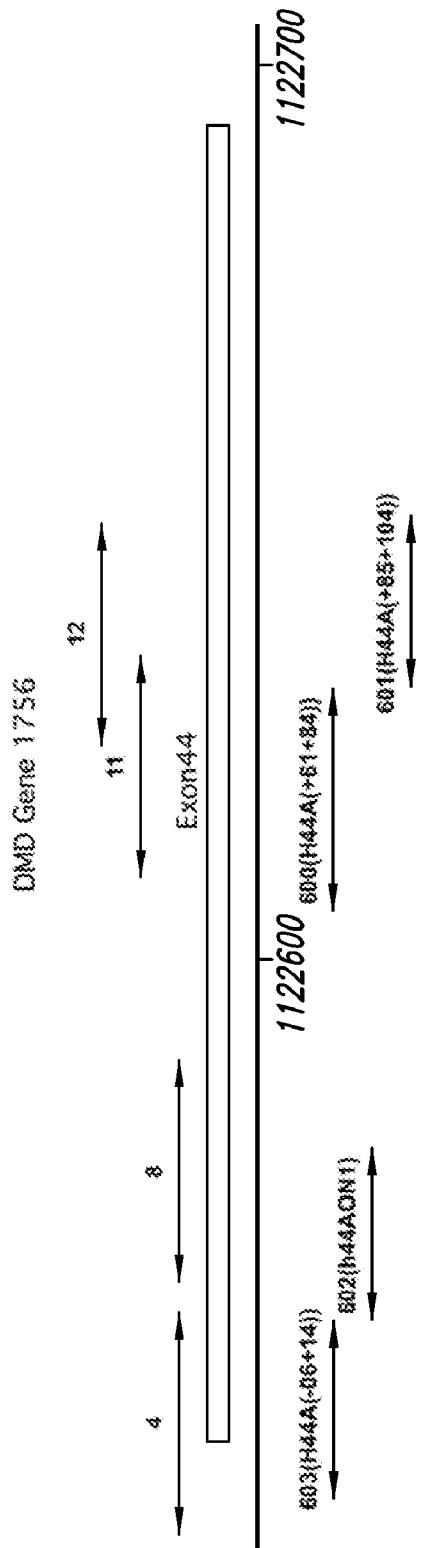


FIG. 5B

Exon 44 DR.2 (Dose-Range)

High-Purity Synthesis, (0.1, 0.3, 1.0, 3.0, 10.0 μ M) RD Cells

NG-08-0792 09AU11-J(A2) (SEQ ID NO: 4)

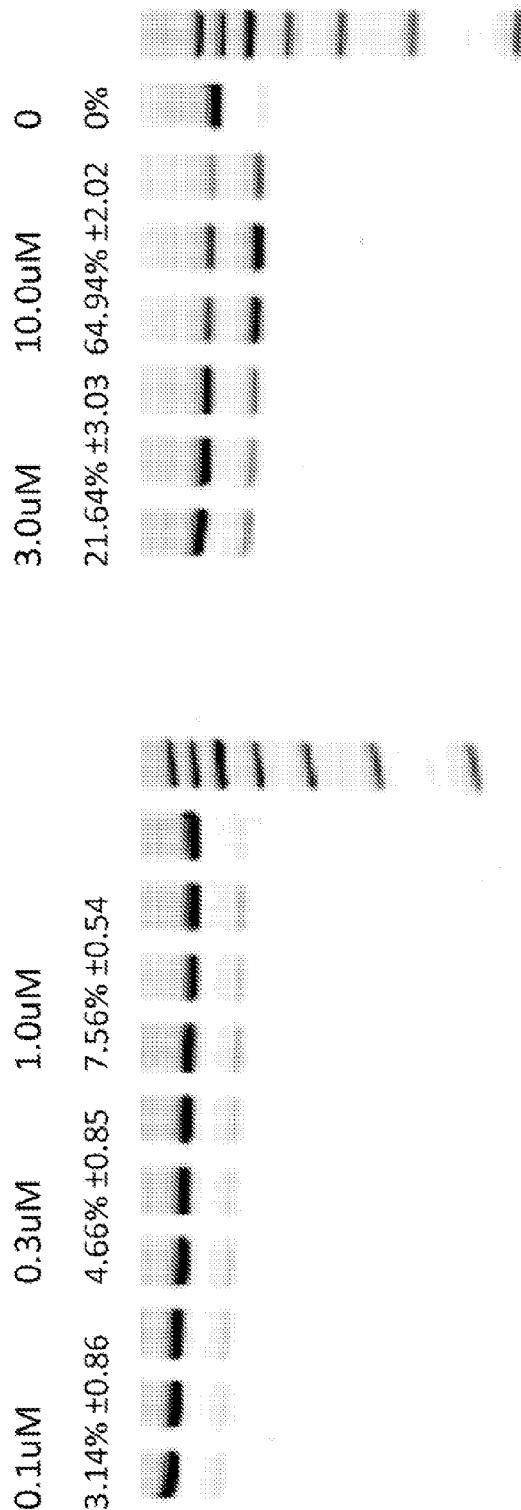


FIG. 5C

ExOn 44 DR.2

High-Purity Synthesis, (0.1, 0.3, 1.0, 3.0, 10.0 μ M) RD Cells

NG-08-0796 09AU11-J(B2) (SEQ ID NO: 8)

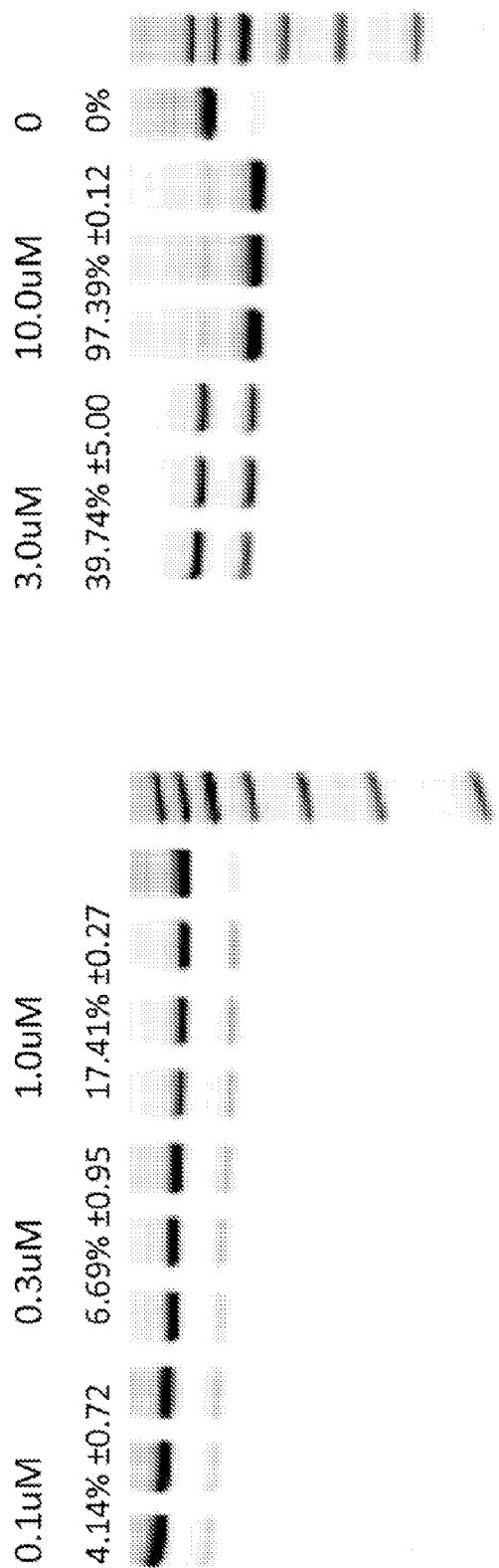


FIG. 5D

ExOn 44 DR.2

High-Purity Synthesis, (0.1, 0.3, 1.0, 3.0, 10.0 μ M) RD Cells

NG-08-0799 09AU11-J(C2) (SEQ ID NO: 11)

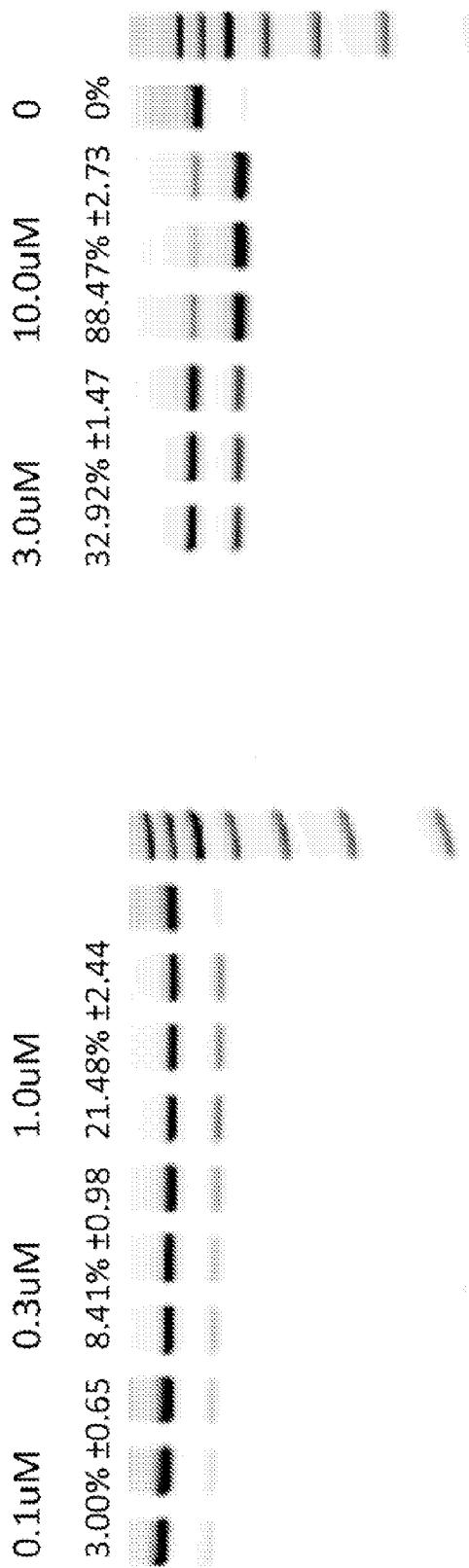


FIG. 5E

Exon 44 DR.2

High-Purity Synthesis, (0.1, 0.3, 1.0, 3.0, 10.0uM) RD Cells

NG-08-0800 09AU11-J(D2) (SEQ ID NO: 12)

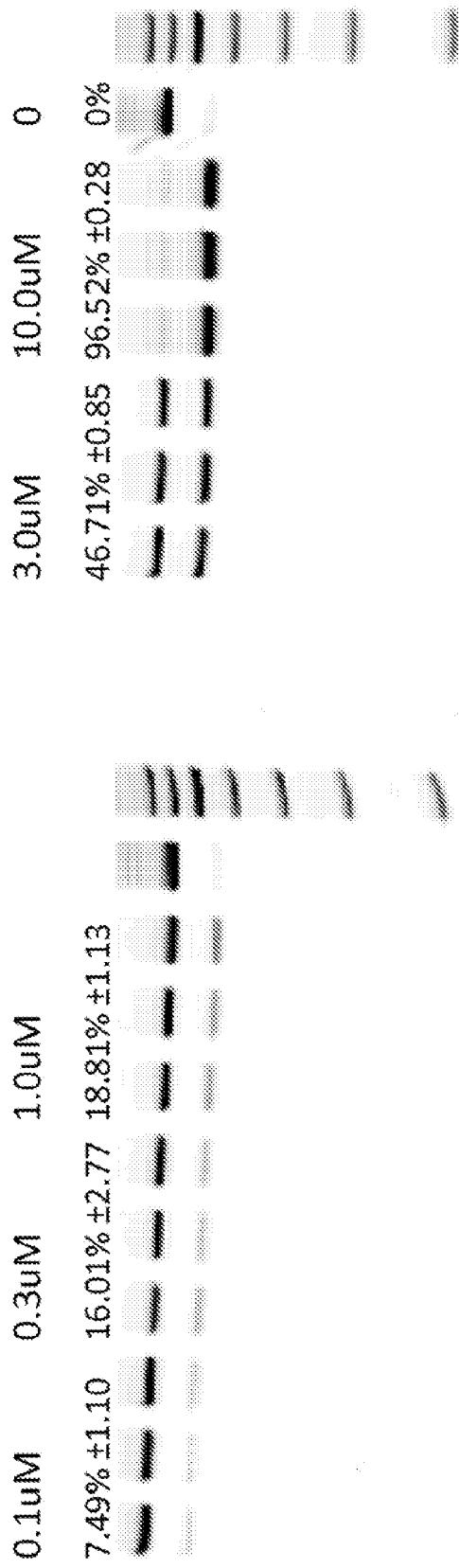


FIG. 5F

Exon 44 DR.2

High-Purity Synthesis, (0.1, 0.3, 1.0, 3.0, 10.0μM) RD Cells

NG-080109AU11-J(E2) (SEQ ID NO: 13)

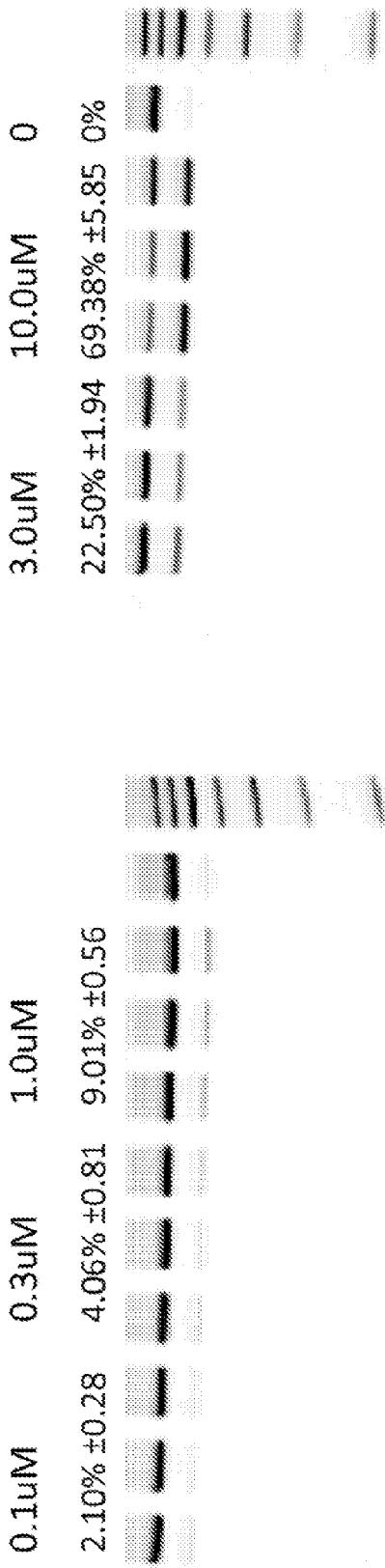


FIG. 5G

Exon44 RD Cell Dose-Range Summary

Treatment (μ M)	Percent Exon Skipped				
	792 (SEQ ID N0:4)	796 (SEQ ID N0:8)	799 (SEQ ID N0:11)	800 (SEQ ID N0:12)	801 (SEQ ID N0:13)
0.1	3.14	4.14	3.00	7.49	2.10
0.3	4.66	6.69	8.41	16.01	4.06
1	7.56	17.41	21.48	18.81	9.01
3	21.64	39.74	32.92	46.71	22.50
10	64.94	97.39	88.47	96.52	69.38
EC ₅₀ (μ M)	7.166	3.024	3.594	2.795	6.277

FIG. 5H

Exon 44 CS (Competitor Screen)

High-Purity Synthesis, 3.0uM, RD Cells

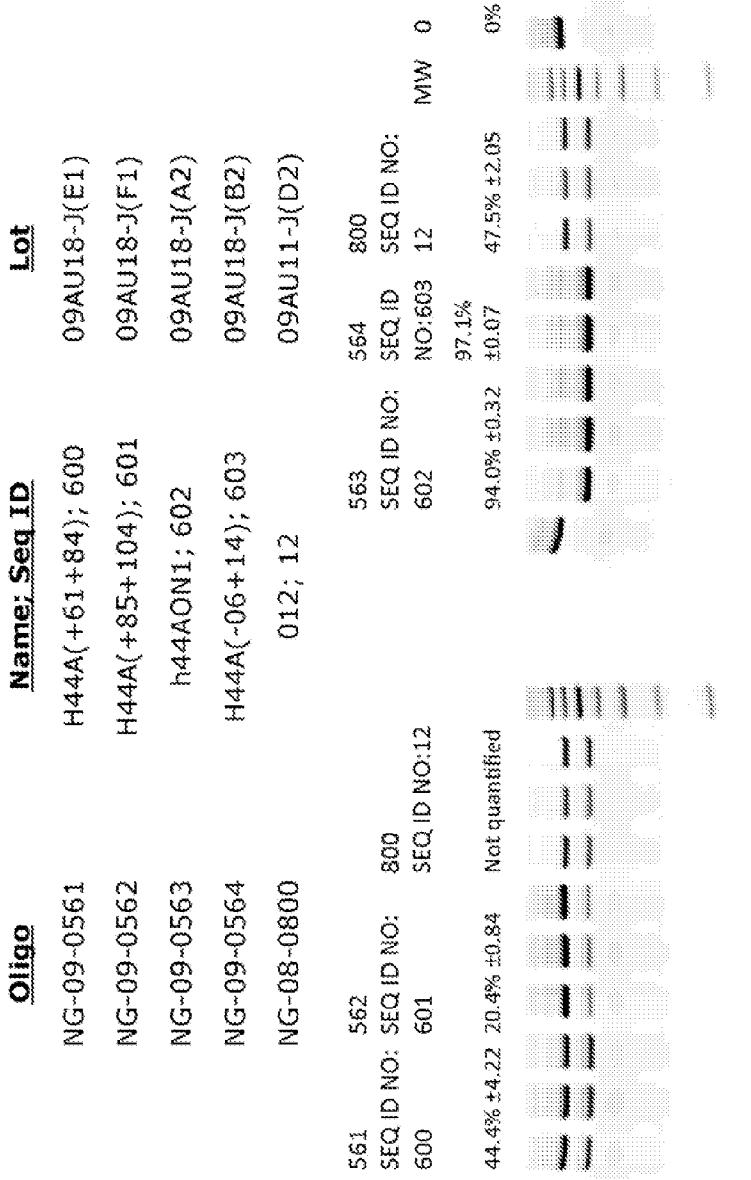


FIG. 5I

Exon 44 MCS (Muscle Cell Competitor Screen)

High-Purity Synthesis, 3.0uM, Human Primary Skeletal Muscle Cells

Oligo	Name: Seq ID	Lot
NG-09-0561	H44A(+61+84); 600	09AU18-J(E1)
NG-09-0562	H44A(+85+104); 601	09AU18-J(F1)
NG-09-0563	n44AON1; 602	09AU18-J(A2)
NG-09-0564	H44A(-06+14); 603	09AU18-J(B2)
NG-08-0800	012; 12	09AU11-J(D2)

Inadequate NG-09-0564 to include in screen.

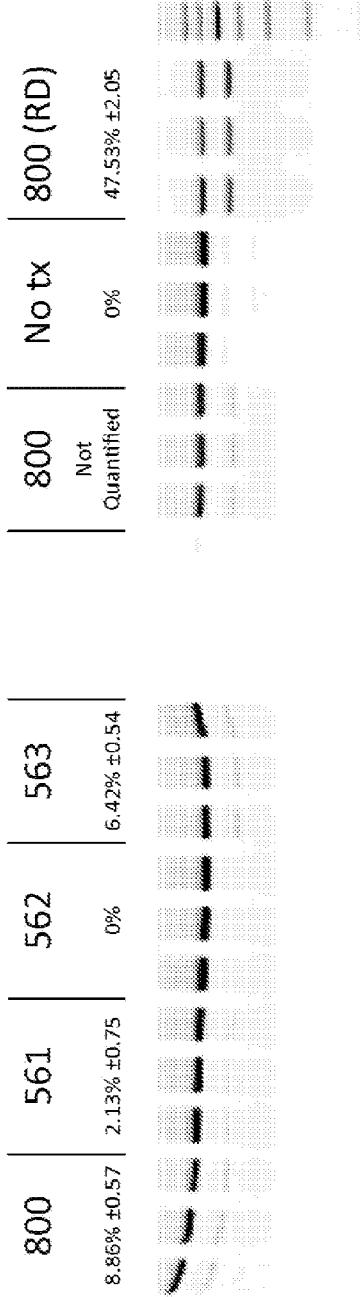


FIG. 5J

Dystrophin Exon 45 Scan Oligos

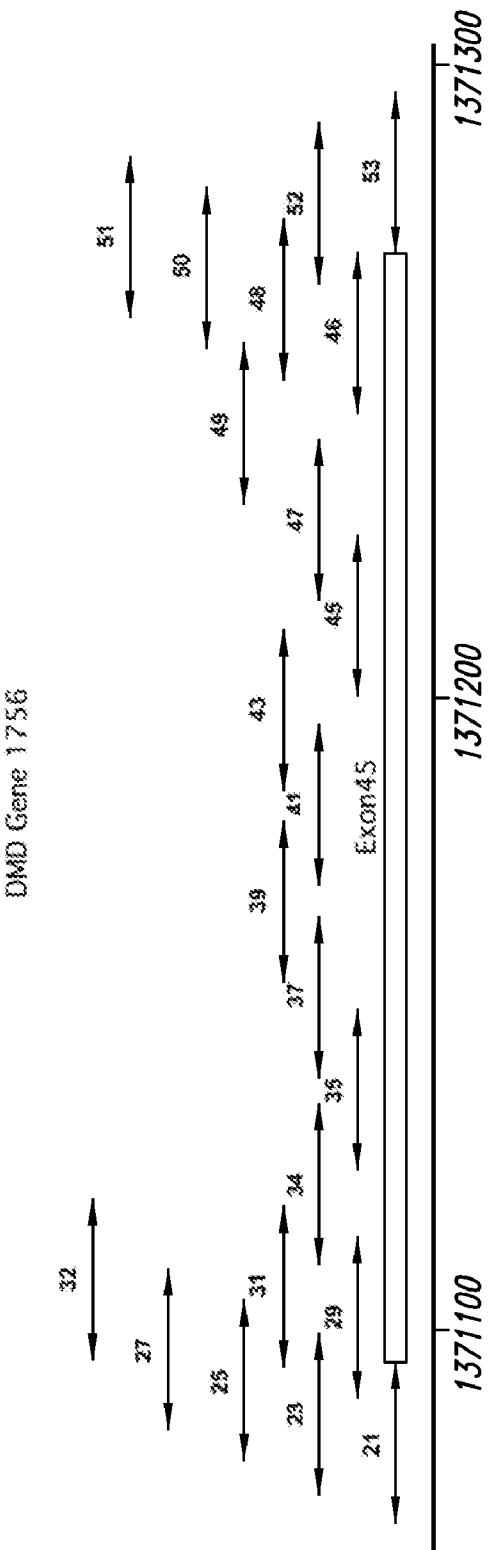


FIG. 6A

Selected Dystrophin Exon 45 Oligos

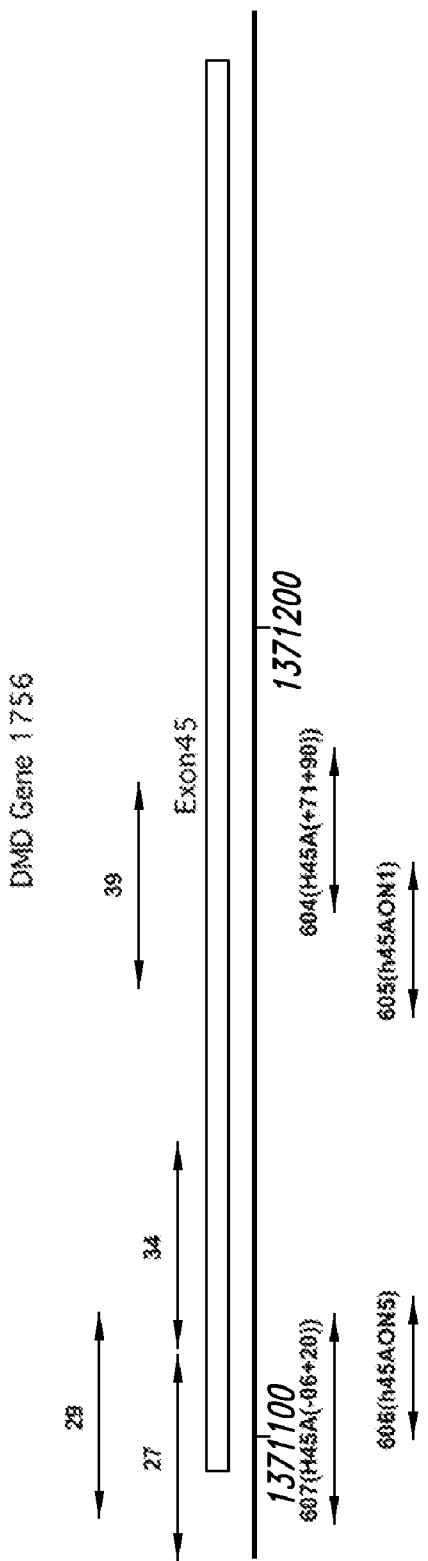


FIG. 6B

Exon 45 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0uM) RD Cells

NG-0770 09AU11-J(F2) (SEQ ID NO: 27)

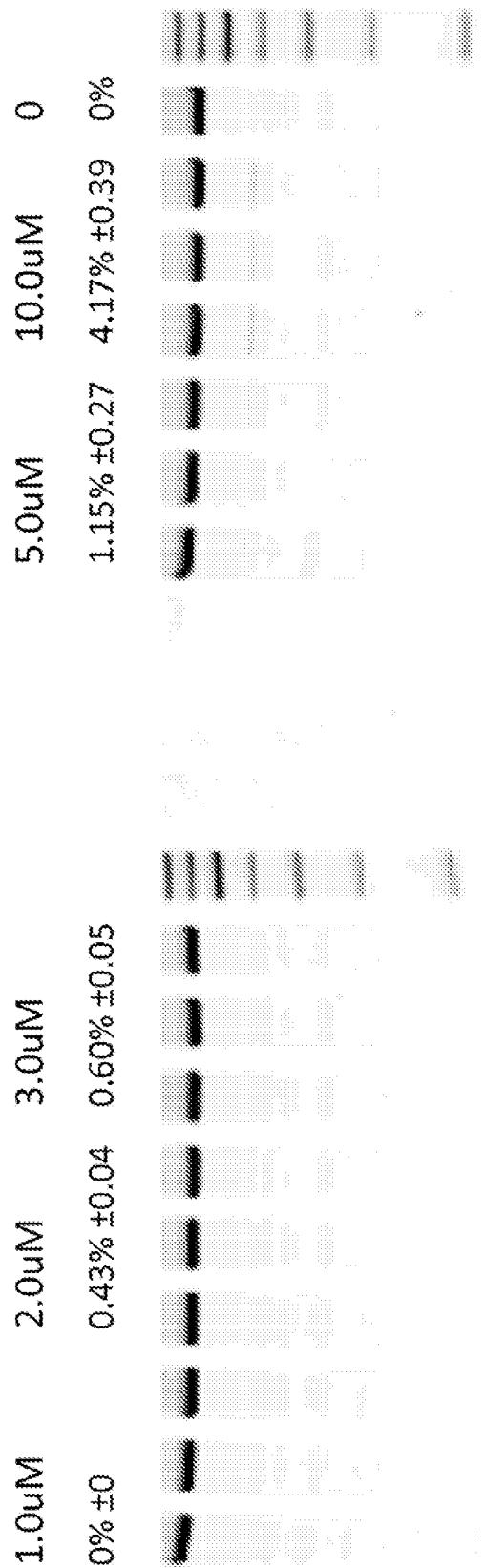


FIG. 6C

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Exon 45 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0uM) RD Cells

NG-0771 09AU11-1(A4) (SEQ ID NO: 29)

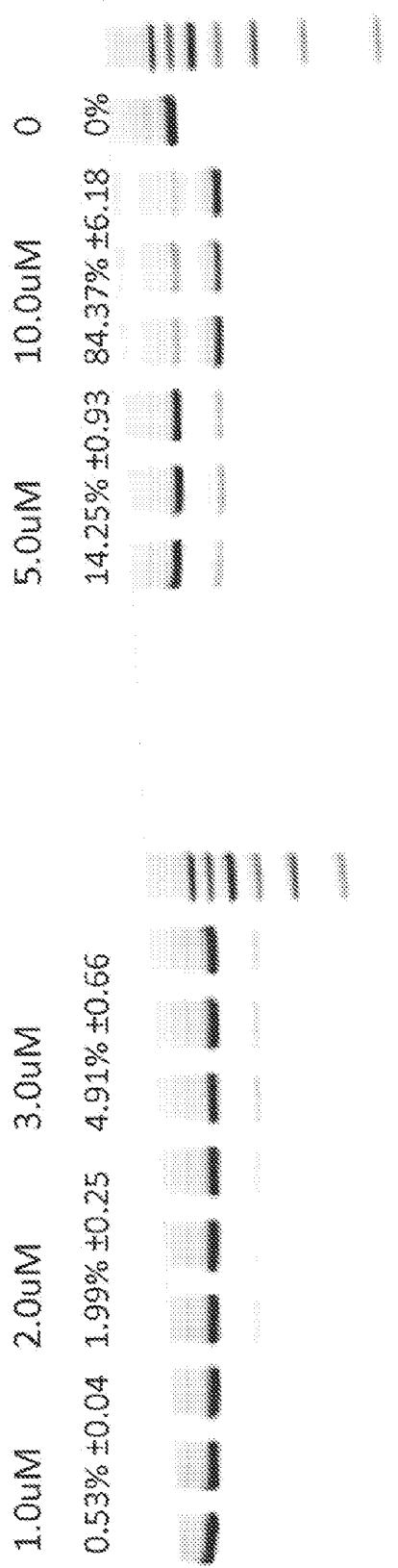


FIG. 6D

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ExOn 45 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0uM) RD Cells

NG-0774 09AU11-J(B4) (SEQ ID NO: 34)

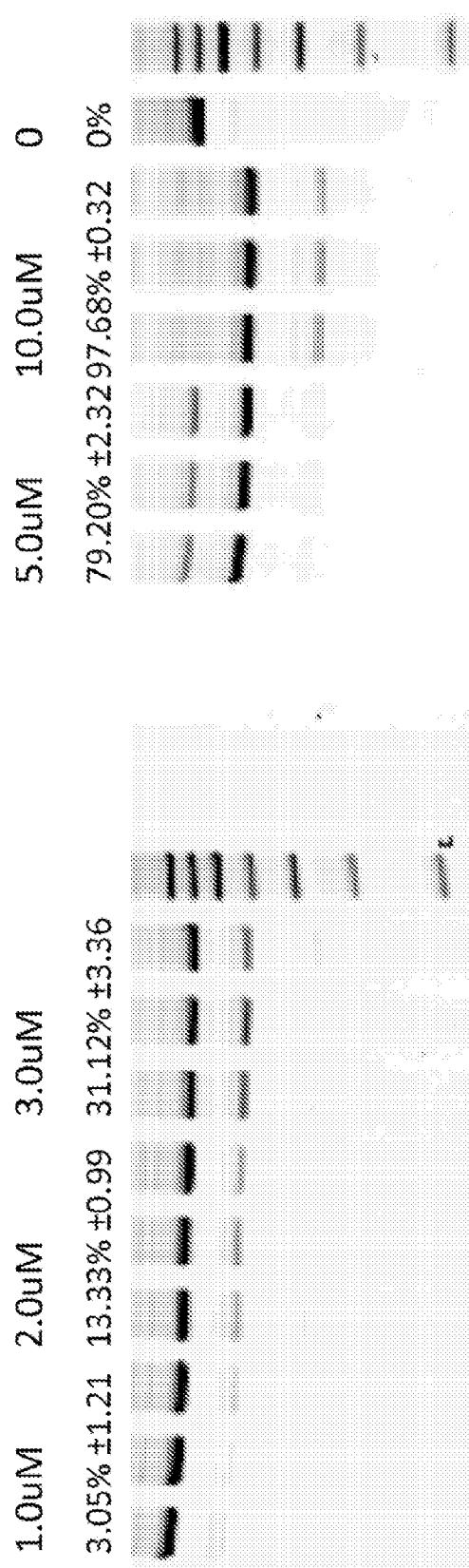


FIG. 6E

Exon 45 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0 μ M) RD Cells

NG-0777 09AU11-J(C4) (SEQ ID NO: 39)

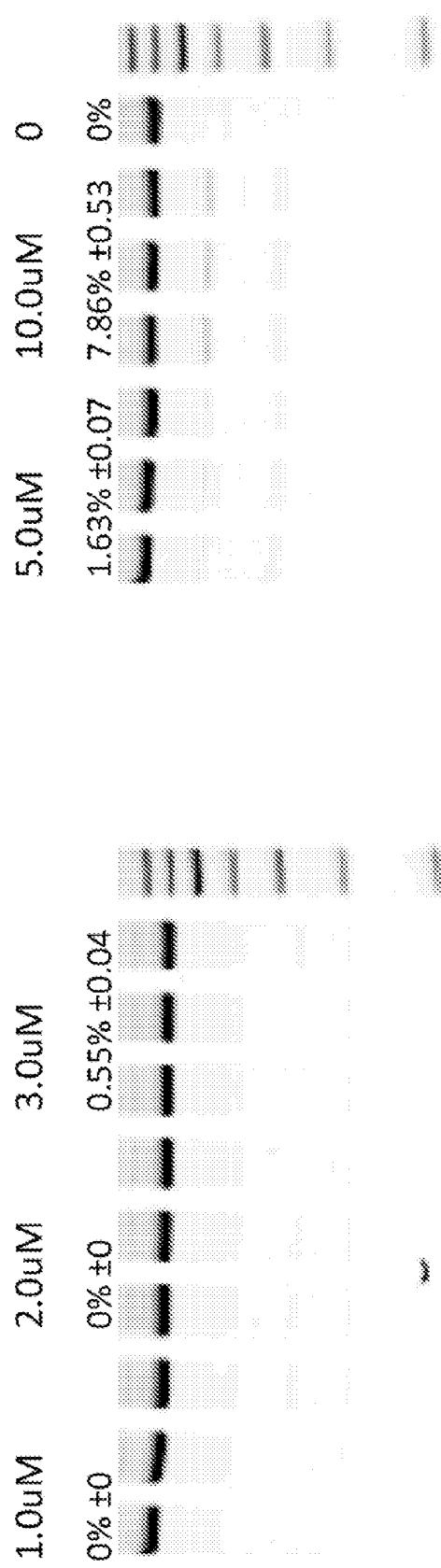


FIG. 6F

Exon 45 DR.2

High-Purity Synthesis, (1.0, 2.0, 3.0, 5.0, 10.0uM) RD Cells

(Negative control)

NG-0782 09AU11-J(D4) (SEQ ID NO: 49)

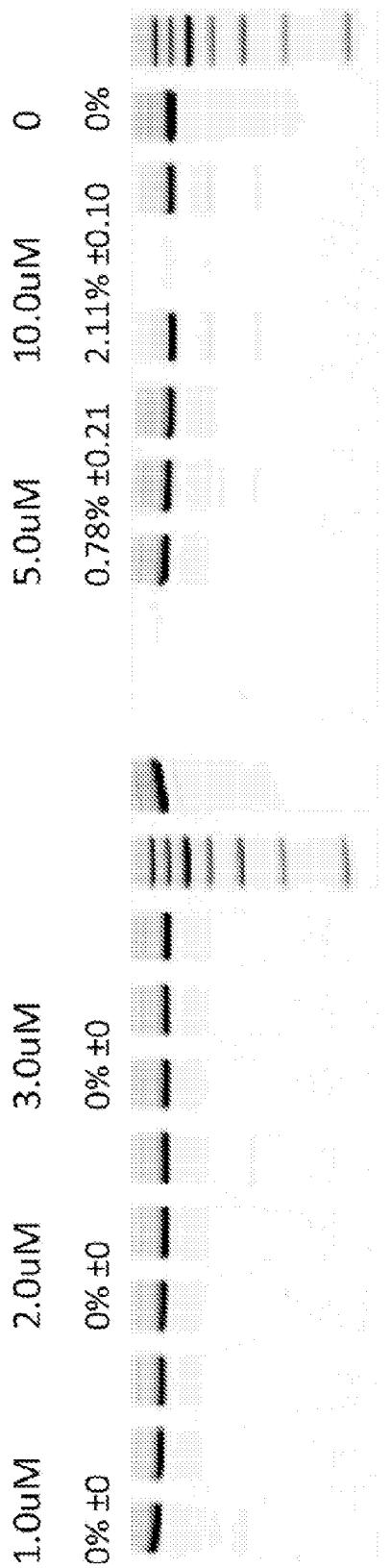


FIG. 6G

Exon45 RD Cell Dose–Range Summary

Treatment (μ M)	Percent Exon Skipped				
	770 (SEQ ID N0:27)	771 (SEQ ID N0:29)	774 (SEQ ID N0:34)	777 (SEQ ID N0:39)	782 (SEQ ID N0:49)
1.0	0.00	0.53	3.05	0.00	0.00
2.0	0.43	1.99	13.53	0.00	0.00
3.0	0.60	4.91	31.12	0.55	0.00
5.0	1.15	14.25	79.20	1.63	0.78
10	4.17	84.37	97.68	7.86	2.11
EC ₅₀ (μ M)	54.37	7.25	3.69	NA	NA

FIG. 6H

Exon 45 CS (Competitor Screen)

High-Purity Synthesis, 3.0uM, RD Cells

<u>Oligo</u>	<u>Name; SEQ ID</u>	<u>Lot</u>
NG-09-0565	H45A(+71+90); 604	09AU18-J(C2)
NG-09-0566	h45AON1; 605	09AU18-J(D2)
NG-09-0567	h45AON5; 606	09AU18-J(E2)
NG-09-0568	H45A(-06+20); 607	09AU18-J(F2)
NG-08-0774	008; 34	09AU11-J(B4)

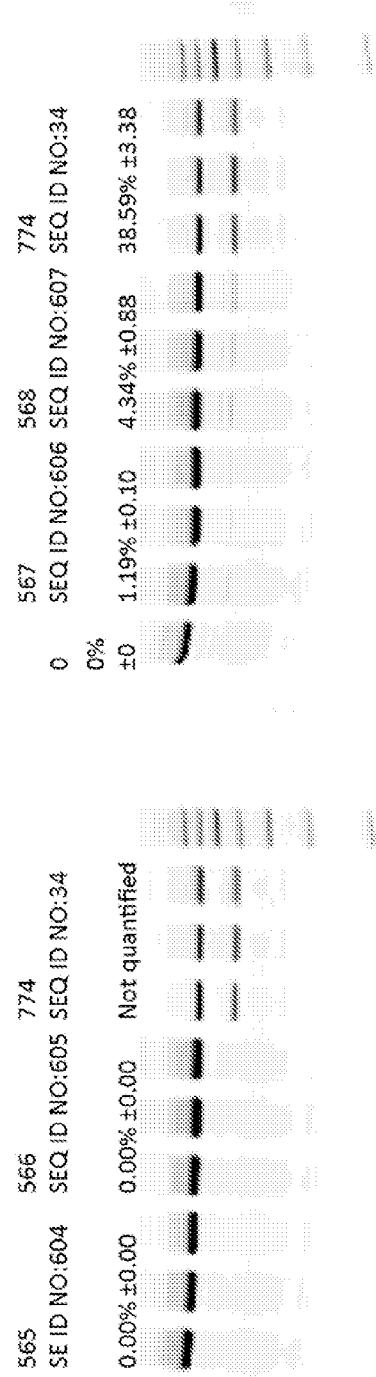


FIG. 6I

Exon 45 MCS (Muscle Cell Competitor Screen)

High-Purity Synthesis, 3.0μM, Human Primary Skeletal Muscle Cells

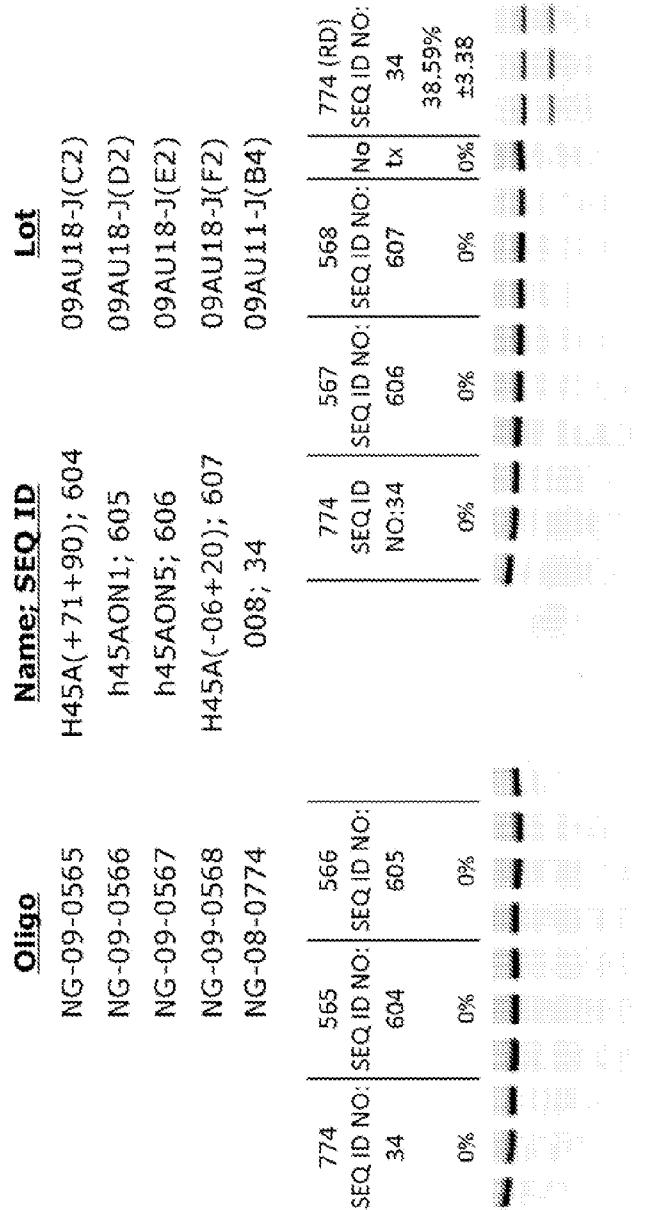


FIG. 6J

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MULTIPLE EXON SKIPPING COMPOSITIONS FOR DMD

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit under 35 U.S.C. §119(e) of U.S. Provisional Patent Application No. 61/108, 416 filed Oct. 24, 2008; wherein this provisional application is incorporated herein by reference in its entirety.

STATEMENT REGARDING SEQUENCE LISTING

[0002] The Sequence Listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is 120178_410_SEQUENCE_LISTING.txt. The text file is 157 KB, was created on Oct. 23, 2009 and is being submitted electronically via EFS-Web.

FIELD OF THE INVENTION

[0003] The present invention relates to novel antisense compounds and compositions suitable for facilitating exon skipping in the human dystrophin gene. It also provides methods for inducing exon skipping using the antisense compositions adapted for use in the methods of the invention.

BACKGROUND OF THE INVENTION

[0004] Antisense technologies are being developed using a range of chemistries to affect gene expression at a variety of different levels (transcription, splicing, stability, translation). Much of that research has focused on the use of antisense compounds to correct or compensate for abnormal or disease-associated genes in a wide range of indications. Antisense molecules are able to inhibit gene expression with specificity, and because of this, many research efforts concerning oligonucleotides as modulators of gene expression have focused on inhibiting the expression of targeted genes or the function of cis-acting elements. The antisense oligonucleotides are typically directed against RNA, either the sense strand (e.g., mRNA) or minus-strand in the case of some viral RNA targets. To achieve a desired effect of specific gene down-regulation, the oligonucleotides generally either promote the decay of the targeted mRNA, block translation of the mRNA or block the function of cis-acting RNA elements thereby effectively preventing either de novo synthesis of the target protein or replication of the viral RNA.

[0005] However, such techniques are not useful where the object is to up-regulate production of the native protein or compensate for mutations that induce premature termination of translation such as nonsense or frame-shifting mutations. In these cases, the defective gene transcript should not be subjected to targeted degradation or steric inhibition, so the antisense oligonucleotide chemistry should not promote target mRNA decay or block translation.

[0006] In a variety of genetic diseases, the effects of mutations on the eventual expression of a gene can be modulated through a process of targeted exon skipping during the splicing process. The splicing process is directed by complex multi-component machinery that brings adjacent exon-intron junctions in pre-mRNA into close proximity and performs cleavage of phosphodiester bonds at the ends of the introns with their subsequent reformation between exons that are to

be spliced together. This complex and highly precise process is mediated by sequence motifs in the pre-mRNA that are relatively short semi-conserved RNA segments to which bind the various nuclear splicing factors that are then involved in the splicing reactions. By changing the way the splicing machinery reads or recognizes the motifs involved in pre-mRNA processing, it is possible to create differentially spliced mRNA molecules. It has now been recognized that the majority of human genes are alternatively spliced during normal gene expression, although the mechanisms involved have not been identified.

[0007] In cases where a normally functional protein is prematurely terminated because of mutations therein, a means for restoring some functional protein production through antisense technology has been shown to be possible through intervention during the splicing processes, and that if exons associated with disease-causing mutations can be specifically deleted from some genes, a shortened protein product can sometimes be produced that has similar biological properties of the native protein or has sufficient biological activity to ameliorate the disease caused by mutations associated with the exon (Sierakowska, Sambade et al. 1996; Wilton, Lloyd et al. 1999; van Deutekom, Bremmer-Bout et al. 2001; Lu, Mann et al. 2003; Aartsma-Rus, Janson et al. 2004). Kole et al. (U.S. Pat. Nos. 5,627,274; 5,916,808; 5,976,879; and 5,665,593) disclose methods of combating aberrant splicing using modified antisense oligonucleotide analogs that do not promote decay of the targeted pre-mRNA. Bennett et al (U.S. Pat. No. 6,210,892) describe antisense modulation of wild-type cellular mRNA processing also using antisense oligonucleotide analogs that do not induce RNase H-mediated cleavage of the target RNA.

[0008] The process of targeted exon skipping is likely to be particularly useful in long genes where there are many exons and introns, where there is redundancy in the genetic constitution of the exons or where a protein is able to function without one or more particular exons. Efforts to redirect gene processing for the treatment of genetic diseases associated with truncations caused by mutations in various genes have focused on the use of antisense oligonucleotides that either: (1) fully or partially overlap with the elements involved in the splicing process; or (2) bind to the pre-mRNA at a position sufficiently close to the element to disrupt the binding and function of the splicing factors that would normally mediate a particular splicing reaction which occurs at that element.

[0009] Duchenne muscular dystrophy (DMD) is caused by a defect in the expression of the protein dystrophin. The gene encoding the protein contains 79 exons spread out over more than 2 million nucleotides of DNA. Any exonic mutation that changes the reading frame of the exon, or introduces a stop codon, or is characterized by removal of an entire out of frame exon or exons or duplications of one or more exons has the potential to disrupt production of functional dystrophin, resulting in DMD.

[0010] A less severe form of muscular dystrophy, Becker muscular dystrophy (BMD) has been found to arise where a mutation, typically a deletion of one or more exons, results in a correct reading frame along the entire dystrophin transcript, such that translation of mRNA into protein is not prematurely terminated. If the joining of the upstream and downstream exons in the processing of a mutated dystrophin pre-mRNA maintains the correct reading frame of the gene, the result is an mRNA coding for a protein with a short internal deletion that retains some activity resulting in a Becker phenotype.

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[0011] Deletions of an exon or exons which do not alter the reading frame of a dystrophin protein give rise to a BMD phenotype, whereas an exon deletion that causes a frame-shift will give rise to DMD (Monaco, Bertelson et al. 1988). In general, dystrophin mutations including point mutations and exon deletions that change the reading frame and thus interrupt proper protein translation result in DMD. It should also be noted that some BMD and DMD patients have exon deletions covering multiple exons.

[0012] Although antisense molecules may provide a tool in the treatment of Duchenne Muscular Dystrophy (DMD), attempts to induce exon skipping using antisense molecules have had mixed success. Successful skipping of dystrophin exon 19 from the dystrophin pre-mRNA was achieved using a variety of antisense molecules directed at the flanking splice sites or motifs within the exon involved in exon definition as described by Errington et al., (Errington, Mann et al. 2003).

[0013] The first example of specific and reproducible exon skipping in the mdx mouse model was reported by Wilton et al (Wilton, Lloyd et al. 1999). By directing an antisense molecule to the donor splice site, exon 23 skipping was induced in the dystrophin mRNA within 6 hours of treatment of the cultured cells. Wilton et al also describe targeting the acceptor region of the mouse dystrophin pre-mRNA with longer antisense oligonucleotides. While the first antisense oligonucleotide directed at the intron 23 donor splice site induced exon skipping in primary cultured myoblasts, this compound was found to be much less efficient in immortalized cell cultures expressing higher levels of dystrophin.

[0014] Despite these efforts, there remains a need for improved antisense oligomers targeted to multiple dystrophin exons and improved muscle delivery compositions and methods for DMD therapeutic applications.

BRIEF SUMMARY OF THE INVENTION

[0015] Embodiments of the present invention relate generally to antisense compounds capable of binding to a selected target to induce exon skipping, and methods of use thereof to induce exon skipping. In certain embodiments, it is possible to combine two or more antisense oligonucleotides of the present invention together to induce single or multiple exon skipping.

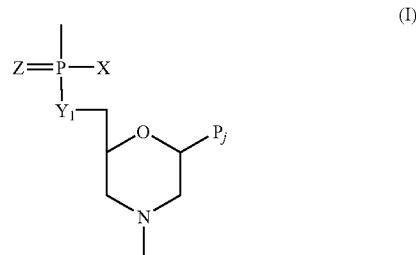
[0016] In certain embodiments, it is possible to improve exon skipping of a single or multiple exons by covalently linking together two or more antisense oligonucleotide molecules (see, e.g., Aartsma-Rus, Janson et al. 2004).

[0017] In certain embodiments, the antisense compounds of the present invention induce exon skipping in the human dystrophin gene, and thereby allow muscle cells to produce a functional dystrophin protein.

[0018] The antisense oligonucleotide compounds (also referred to herein as oligomers) of the present invention typically: (i) comprise morpholino subunits and phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, (ii) contain between 10-40 nucleotide bases, preferably 20-35 bases (iii) comprise a base sequence effective to hybridize to at least 12 contiguous bases of a target sequence in dystrophin pre-mRNA and induce exon skipping.

[0019] In certain embodiments, the antisense compounds of the present invention may comprise phosphorus-containing intersubunit linkages joining a morpholino nitrogen of

one subunit to a 5' exocyclic carbon of an adjacent subunit, in accordance with the following structure (I):



wherein:

[0020] Y₁ is —O—, —S—, —NH—, or —CH₂—;

[0021] Z is O or S;

[0022] Pj is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide; and

[0023] X is fluoro, optionally substituted alkoxy, optionally substituted thioalkoxy, amino, optionally substituted alkylamino, or optionally substituted heterocyclyl.

[0024] In certain embodiments, the above intersubunit linkages, which are uncharged, may be interspersed with linkages that are positively charged at physiological pH, where the total number of positively charged linkages is between 2 and no more than half of the total number of linkages. For example, the positively charged linkages may have the above structure in which X is optionally substituted 1-piperazinyl. In other embodiments, the positively charged linkages may have the above structure in which X is substituted 1-piperazinyl, wherein the 1-piperazinyl is substituted at the 4-position with an optionally substituted alkyl guanidinyl moiety.

[0025] Where the antisense compound administered is effective to target a splice site of preprocessed human dystrophin, it may have a base sequence complementary to a target region containing at least 12 contiguous bases in a preprocessed messenger RNA (mRNA) human dystrophin transcript. Exemplary antisense sequences include those identified by SEQ ID NOS: 1 to 569 and 612 to 633.

[0026] In certain embodiments, an antisense sequence of the present invention is contained within:

[0027] (a) any of the sequences identified by SEQ ID NOS: 1-20, preferably SEQ ID NOS: 4, 8, 11 and 12, and more preferably SEQ ID NO:12 for use in producing skipping of exon 44 in the processing of human dystrophin pre-processed mRNA;

[0028] (b) any of the sequences identified by SEQ ID NOS: 21-76 and 612 to 624, preferably SEQ ID NOS: 27, 29, 34 and 39, and more preferably SEQ ID NO: 34 for use in producing skipping of exon 45 in the processing of human dystrophin pre-processed mRNA;

[0029] (c) any of the sequences identified by SEQ ID NOS: 77-125, preferably SEQ ID NOS: 21 to 53, and more preferably SEQ ID NOS: 82, 84-87, 90 96, 98, 99 and 101, for use in producing skipping of exon 46 in the processing of human dystrophin pre-processed mRNA;

[0030] (d) any of the sequences identified by SEQ ID NOS: 126-169, preferably SEQ ID NOS: 126-149, and more preferably SEQ ID NOS: 126, 128-130, 132, 144 and 146-149, for use in producing skipping of exon 47 in the processing of human dystrophin pre-processed mRNA;

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[0031] (e) any of the sequences identified by SEQ ID NOS: 170-224 and 634, preferably SEQ ID NOS: 170-201 and 634, and more preferably SEQ ID NOS: 176, 178, 181-183, 194 and 198-201, for use in producing skipping of exon 48 in the processing of human dystrophin pre-processed mRNA;

[0032] (f) any of the sequences identified by SEQ ID NOS: 225-266, preferably SEQ ID NOS: 225-248, and more preferably SEQ ID NOS: 227, 229, 234, 236, 237 and 244-248, for use in producing skipping of exon 49 in the processing of human dystrophin pre-processed mRNA;

[0033] (g) any of the sequences identified by SEQ ID NOS: 267-308, preferably SEQ ID NOS: 277, 287 and 290, and more preferably SEQ ID NO: 287, for use in producing skipping of exon 50 in the processing of human dystrophin pre-processed mRNA;

[0034] (h) any of the sequences identified by SEQ ID NOS: 309-371, preferably SEQ ID NOS: 324, 326 and 327, and more preferably SEQ ID NO: 327 for use in producing skipping of exon 51 in the processing of human dystrophin pre-processed mRNA;

[0035] (i) any of the sequences identified by SEQ ID NOS: 372-415, preferably SEQ ID NOS: 372-397, and more preferably SEQ ID NOS: 379-382, 384, 390 and 392-395 for use in producing skipping of exon 52 in the processing of human dystrophin pre-processed mRNA;

[0036] (j) any of the sequences identified by SEQ ID NOS: 416-475 and 625-633, preferably SEQ ID NOS: 428, 429 and 431, and more preferably SEQ ID NO: 429, for use in producing skipping of exon 53 in the processing of human dystrophin pre-processed mRNA;

[0037] (k) any of the sequences identified by SEQ ID NOS: 476-519, preferably SEQ ID NOS: 476-499, and more preferably SEQ ID NOS: 479-482, 484, 489 and 491-493, for use in producing skipping of exon 54 in the processing of human dystrophin pre-processed mRNA; and

[0038] (l) any of the sequences identified by SEQ ID NOS: 520-569 and 635, preferably SEQ ID NOS: 520-546 and 635, and more preferably SEQ ID NOS: 524-528, 537, 539, 540, 542 and 544, for use in producing skipping of exon 55 in the processing of human dystrophin pre-processed mRNA;

[0039] In certain embodiments, the compound may be conjugated to an arginine-rich polypeptide effective to promote uptake of the compound into cells. Exemplary peptides include those identified by SEQ ID NOS: 570 to 578, among others described herein.

[0040] In one exemplary embodiment, the arginine-rich polypeptide is covalently coupled at its N-terminal or C-terminal residue to the 3' or 5' end of the antisense compound. Also in an exemplary embodiment, the antisense compound is composed of morpholino subunits and phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit.

[0041] In general, the peptide-oligomer conjugate may further comprise a homing peptide which is selective for a selected mammalian tissue, i.e., the same tissue being targeted by the cell-penetrating peptide. The conjugate may be of the form: cell penetrating peptide-homing peptide-antisense oligomer, or, more preferably, of the form: homing peptide-cell penetrating peptide-antisense oligomer. For example, a peptide conjugate compound for use in treating Duchenne muscular dystrophy, as described above, can further comprise a homing peptide which is selective for muscle tissue, such as the peptide having the sequence identified as SEQ ID NO: 579, conjugated to the cell-penetrating peptide.

Exemplary conjugates of this type include those represented herein as CP06062-MSP-PMO (cell penetrating peptide-homing peptide-antisense oligomer) and as MSP-CP06062-PMO (homing peptide-cell penetrating peptide-antisense oligomer) (see SEQ ID NOs: 580-583).

[0042] In some embodiments, the peptide is conjugated to the oligomer via a linker moiety. In certain embodiments the linker moiety may comprise an optionally substituted piperazinyl moiety. In other embodiments, the linker moiety may further comprise a beta alanine and/or a 6-aminoheptanoic acid subunit. In yet other embodiments, the peptide is conjugated directly to the oligomer without a linker moiety.

[0043] Conjugation of the peptide to the oligomer may be at any position suitable for forming a covalent bond between the peptide and the oligomer or between the linker moiety and the oligomer. For example, in some embodiments conjugation of the peptide may be at the 3' end of the oligomer. In other embodiments, conjugation of the peptide to the oligomer may be at the 5' end of the oligomer. In yet other embodiments, the peptide may be conjugated to the oligomer through any of the intersubunit linkages.

[0044] In some embodiments, the peptide is conjugated to the oligomer at the 5' end of the oligomer. In embodiments comprising phosphorus-containing intersubunit linkages, the peptide may be conjugated to the oligomer via a covalent bond to the phosphorous of the terminal linkage group. Conjugation in this manner may be with or without the linker moiety described above.

[0045] In yet other embodiments, the peptide may be conjugated to the oligomer at the 3' end of the oligomer. In some further embodiments, the peptide may be conjugated to the nitrogen atom of the 3' terminal morpholino group of the oligomer. In this respect, the peptide may be conjugated to the oligomer directly or via the linker moiety described above.

[0046] In some embodiments, the oligomer may be conjugated to a moiety that enhances the solubility of the oligomer in aqueous medium. In some embodiments, the moiety that enhances solubility of the oligomer in aqueous medium is a polyethyleneglycol. In yet further embodiments, the moiety that enhances solubility of the oligomer in aqueous medium is triethylene glycol. For example, in some embodiments the moiety that enhances solubility in aqueous medium may be conjugated to the oligomer at the 5' end of the oligomer. Conjugation of the moiety that enhances solubility of the oligomer in aqueous medium to the oligomer may be either directly or through the linker moiety described above.

[0047] Certain embodiments of the present invention provide antisense molecules selected and/or adapted to aid in the prophylactic or therapeutic treatment of a genetic disorder comprising at least an antisense molecule in a form suitable for delivery to a patient.

[0048] Certain embodiments of the invention provide methods for treating a patient suffering from a genetic disease wherein there is a mutation in a gene encoding a particular protein and the effect of the mutation can be abrogated by exon skipping, comprising the steps of: (a) selecting an antisense molecule in accordance with the methods described herein; and (b) administering the molecule to a patient in need of such treatment. The present invention also includes the use of purified and isolated antisense oligonucleotides of the invention, for the manufacture of a medicament for treatment of a genetic disease.

[0049] Certain embodiments provide a method of treating muscular dystrophy, such as a condition characterized by

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Duchenne muscular dystrophy, which method comprises administering to a patient in need of treatment an effective amount of an appropriately designed antisense oligonucleotide, as described herein, relevant to the particular genetic lesion in that patient. Further, certain embodiments provide a method for prophylactically treating a patient to prevent or at least minimize muscular dystrophy, including Duchene muscular dystrophy, comprising the step of: administering to the patient an effective amount of an antisense oligonucleotide or a pharmaceutical composition comprising one or more of these biological molecules.

[0050] Certain embodiments relate to methods of treating muscular dystrophy in a subject, comprising administering to the subject an effective amount of a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 1 to 569 and 612 to 635, and capable of forming with the complementary mRNA sequence in a dystrophin-gene exon a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C., wherein the exon is selected from the group consisting of exons 44-55.

[0051] In certain embodiments, the muscular dystrophy is Duchenne's muscular dystrophy (DMD). In certain embodiments, the muscular dystrophy is Becker muscular dystrophy (BMD).

[0052] In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 1-20, and the exon is exon 44. In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 21-76 and 612 to 624, and the exon is exon 45.

[0053] In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 77-125, and the exon is exon 46. In certain embodiments, the sequence selected from the group consisting SEQ ID NOS: 126-169, and the exon is exon 47.

[0054] In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 170-224 and 634, and the exon is exon 48. In certain embodiments, the sequence selected from the group consisting SEQ ID NOS: 225-266, and the exon is exon 49.

[0055] In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 267-308, and the exon is exon 50. In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 309-371, and the exon is exon 51.

[0056] In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 372-415, and the exon is exon 52. In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 416-475 and 625-633, and the exon is exon 53. In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 476-519, and the exon is exon 54. In certain embodiments, the sequence is selected from the group consisting SEQ ID NOS: 520-569 and 635, and the exon is exon 55. In certain embodiments, the sequence comprises or consists essentially of SEQ ID NO:287.

[0057] Certain embodiments provide kits for treating a genetic disease, which kits comprise at least an antisense oligonucleotide of the present invention, packaged in a suitable container and instructions for its use.

[0058] These and other objects and features will be more fully understood when the following detailed description of the invention is read in conjunction with the figures.

BRIEF DESCRIPTION OF THE FIGURES

[0059] FIG. 1A shows an exemplary morpholino oligomer structure with a phosphorodiamidate linkage;

[0060] FIG. 1B shows a conjugate of an arginine-rich peptide and an antisense oligomer, in accordance with an embodiment of the invention;

[0061] FIG. 1C shows a conjugate as in FIG. 1B, wherein the backbone linkages contain one or more positively charged groups;

[0062] FIGS. 1D-G show the repeating subunit segment of exemplary morpholino oligonucleotides, designated D through G.

[0063] FIG. 2A shows the relative location and results of an antisense oligomer exon 51 scan designed to induce skipping of human dystrophin exon 51.

[0064] FIG. 2B-C shows the relative activity in cultured human rhabdomyosarcoma (RD) cells and human primary skeletal muscle cells of the three best oligomers selected from the exon 51 scan (SEQ ID NOS: 324, 326 and 327) relative to sequences (AVI-5658; SEQ ID NO: 588 and h51AON1; SEQ ID NO:594) that are effective at inducing exon 51 skipping.

[0065] FIG. 2D shows the relative location within exon 51 of three selected oligomers compared to certain sequences.

[0066] FIG. 3A shows the relative location and results of an antisense oligomer exon 50 scan designed to induce skipping of human dystrophin exon 50 compared to other sequences that induce exon 50 skipping.

[0067] FIG. 3B shows the relative location and activity of antisense sequences selected from the exon 50 scan (SEQ ID NOS: 277, 287, 290 and 291) compared to other sequences (SEQ ID NOS: 584 and 585).

[0068] FIG. 4A shows the relative location and results of an antisense oligomer exon 53 scan designed to induce skipping of human dystrophin exon 53.

[0069] FIG. 4B shows the relative location of certain sequences used to compare the exon-skipping activity of those oligomers selected as being most active in the exon 53 scan.

[0070] FIGS. 4C-F show the results of dose-ranging studies, summarized in

[0071] FIG. 4G, using the oligomers selected as being most efficacious in the exon 53 scan (SEQ ID NOS:422, 428, 429 and 431).

[0072] FIGS. 4H and 4I show the relative activity of certain sequences (SEQ ID NOS: 608-611) compared to the activity of the most active exon 53-skipping oligomer (SEQ ID NO:429) in both RD cells and human primary skeletal muscle cells.

[0073] FIG. 5A shows the relative location and results of an antisense oligomer exon 44 scan designed to induce skipping of human dystrophin exon 44.

[0074] FIG. 5B shows the relative location within exon 44 of certain sequences used to compare the exon-skipping activity to those oligomers selected as being most active in the exon 44 scan.

[0075] FIGS. 5C-G show the results of dose-ranging studies, summarized in

[0076] FIG. 5H, using the oligomers selected as being most efficacious in the exon 44 scan (SEQ ID NOS: 4, 8, 11, 12 and 13).

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[0077] FIGS. 5I and 5J show the relative activity of certain sequences (SEQ ID NOS: 600-603) compared to the activity of the most active exon 53-skipping oligomer (SEQ ID NO:12) in both RD cells and human primary skeletal muscle cells.

[0078] FIG. 6A shows the relative location and results of an antisense oligomer exon 45 scan designed to induce skipping of human dystrophin exon 45.

[0079] FIG. 6B shows the relative location within exon 45 of certain sequences used to compare the exon-skipping activity to those oligomers selected as being most active in the exon 45 scan.

[0080] FIGS. 6C-F show the results of dose-ranging studies, summarized in

[0081] FIG. 6H, using the oligomers selected as being most efficacious in the exon 45 scan (SEQ ID NOS: 27, 29, 34 and 39).

[0082] FIG. 6G uses a relatively inactive oligomer (SEQ ID NO: 49) as a negative control.

[0083] FIGS. 6I and 6J show the relative activity of certain sequences (SEQ ID NOS: 604-607) compared to the activity of the most active exon 53-skipping oligomer (SEQ ID NO: 34) in both RD cells and human primary skeletal muscle cells.

DETAILED DESCRIPTION OF THE INVENTION

[0084] Embodiments of the present invention relate generally to improved antisense compounds, and methods of use thereof, which are specifically designed to induce exon skipping in the dystrophin gene. Dystrophin plays a vital role in muscle function, and various muscle-related diseases are characterized by mutated forms of this gene. Hence, in certain embodiments, the improved antisense compounds described herein induce exon skipping in mutated forms of the human dystrophin gene, such as the mutated dystrophin genes found in Duchenne's muscular dystrophy (DMD) and Becker's muscular dystrophy (BMD).

[0085] Due to aberrant mRNA splicing events caused by mutations, these mutated human dystrophin genes either express defective dystrophin protein or express no measurable dystrophin at all, a condition that leads to various forms of muscular dystrophy. To remedy this condition, the anti-sense compounds of the present invention typically hybridize to selected regions of a pre-processed RNA of a mutated human dystrophin gene, induce exon skipping and differential splicing in that otherwise aberrantly spliced dystrophin mRNA, and thereby allow muscle cells to produce an mRNA transcript that encodes a functional dystrophin protein. In certain embodiments, the resulting dystrophin protein is not necessarily the "wild-type" form of dystrophin, but is rather a truncated, yet functional or semi-functional, form of dystrophin.

[0086] By increasing the levels of functional dystrophin protein in muscle cells, these and related embodiments may be useful in the prophylaxis and treatment of muscular dystrophy, especially those forms of muscular dystrophy, such as DMD and BMD, that are characterized by the expression of defective dystrophin proteins due to aberrant mRNA splicing. The specific oligomers described herein further provide improved, dystrophin-exon-specific targeting over other oligomers in use, and thereby offer significant and practical advantages over alternate methods of treating relevant forms of muscular dystrophy.

[0087] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly

understood by those of ordinary skill in the art to which the invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, preferred methods and materials are described. For the purposes of the present invention, the following terms are defined below.

DEFINITIONS

[0088] The articles "a" and "an" are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

[0089] By "about" is meant a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 30, 25, 20, 25, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1% to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

[0090] By "coding sequence" is meant any nucleic acid sequence that contributes to the code for the polypeptide product of a gene. By contrast, the term "non-coding sequence" refers to any nucleic acid sequence that does not contribute to the code for the polypeptide product of a gene.

[0091] Throughout this specification, unless the context requires otherwise, the words "comprise," "comprises," and "comprising" will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

[0092] By "consisting of" is meant including, and limited to, whatever follows the phrase "consisting of." Thus, the phrase "consisting of" indicates that the listed elements are required or mandatory, and that no other elements may be present. By "consisting essentially of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase "consisting essentially of" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present depending upon whether or not they materially affect the activity or action of the listed elements.

[0093] The terms "complementary" and "complementarity" refer to polynucleotides (i.e., a sequence of nucleotides) related by the base-pairing rules. For example, the sequence "A-G-T," is complementary to the sequence "T-C-A." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. While perfect complementarity is often desired, some embodiments can include one or more but preferably 6, 5, 4, 3, 2, or 1 mismatches with respect to the target RNA. Variations at any location within the oligomer are included. In certain embodiments, variations in sequence near the termini of an oligomer are generally preferable to variations in the interior, and if present are typically within about 6, 5, 4, 3, 2, or 1 nucleotides of the 5' and/or 3' terminus.

[0094] The terms "cell penetrating peptide" or "CPP" are used interchangeably and refer to cationic cell penetrating peptides, also called transport peptides, carrier peptides, or peptide transduction domains. The peptides, as shown herein,

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have the capability of inducing cell penetration within 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% of cells of a given cell culture population, including all integers in between, and allow macromolecular translocation within multiple tissues in vivo upon systemic administration.

[0095] The terms “antisense oligomer” or “antisense compound” are used interchangeably and refer to a sequence of cyclic subunits, each bearing a base-pairing moiety, linked by intersubunit linkages that allow the base-pairing moieties to hybridize to a target sequence in a nucleic acid (typically an RNA) by Watson-Crick base pairing, to form a nucleic acid: oligomer heteroduplex within the target sequence. The cyclic subunits are based on ribose or another pentose sugar or, in a preferred embodiment, a morpholino group (see description of morpholino oligomers below).

[0096] Such an antisense oligomer can be designed to block or inhibit translation of mRNA or to inhibit natural pre-mRNA splice processing, and may be said to be “directed to” or “targeted against” a target sequence with which it hybridizes. In certain embodiments, the target sequence includes a region including an AUG start codon of an mRNA, a 3’ or 5’ splice site of a pre-processed mRNA, or a branch point. The target sequence may be within an exon or within an intron. The target sequence for a splice site may include an mRNA sequence having its 5’ end 1 to about 25 base pairs downstream of a normal splice acceptor junction in a preprocessed mRNA. A preferred target sequence for a splice is any region of a preprocessed mRNA that includes a splice site or is contained entirely within an exon coding sequence or spans a splice acceptor or donor site. An oligomer is more generally said to be “targeted against” a biologically relevant target, such as a protein, virus, or bacteria, when it is targeted against the nucleic acid of the target in the manner described above. Included are antisense oligomers that comprise, consist essentially of, or consist of one or more of SEQ ID NOS:1 to 569 and 612 to 635. Also included are variants of these antisense oligomers, including variant oligomers having 80%, 85%, 90%, 95%, 97%, 98%, or 99% (including all integers in between) sequence identity or sequence homology to any one of SEQ ID NOS:1 to 569 and 612 to 635, and/or variants that differ from these sequences by about 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides, preferably those variants that induce exon skipping of one or more selected human dystrophin exons. Also included are oligomers of any one or more of SEQ ID NOS:584-611 and 634-635, which comprise a suitable number of charged linkages, as described herein, e.g. up to about 1 per every 2-5 uncharged linkages, such as about 4-5 per every 10 uncharged linkages, and/or which comprise an Arg-rich peptide attached thereto, as also described herein.

[0097] The terms “morpholino oligomer” or “PMO” (phosphoramidate- or phosphorodiamidate morpholino oligomer) refer to an oligonucleotide analog composed of morpholino subunit structures, where (i) the structures are linked together by phosphorus-containing linkages, one to three atoms long, preferably two atoms long, and preferably uncharged or cationic, joining the morpholino nitrogen of one subunit to a 5’ exocyclic carbon of an adjacent subunit, and (ii) each morpholino ring bears a purine or pyrimidine base-pairing moiety effective to bind, by base specific hydrogen bonding, to a base in a polynucleotide. See, e.g., the structure in FIG. 1A, which shows a preferred phosphorodiamidate linkage type. Variations can be made to this linkage as long as they do not interfere with binding or activity. For example, the oxygen attached to phosphorus may be substituted with sulfur (thio-

phosphorodiamidate). The 5’ oxygen may be substituted with amino or lower alkyl substituted amino. The pendant nitrogen attached to phosphorus may be unsubstituted, monosubstituted, or disubstituted with (optionally substituted) lower alkyl. See also the discussion of cationic linkages below. The synthesis, structures, and binding characteristics of morpholino oligomers are detailed in U.S. Pat. Nos. 5,698,685, 5,217,866, 5,142,047, 5,034,506, 5,166,315, 5,521,063, and 5,506,337, and PCT Appn. No. PCT/US07/11435 (cationic linkages), all of which are incorporated herein by reference.

[0098] The purine or pyrimidine base pairing moiety is typically adenine, cytosine, guanine, uracil, thymine or inosine. Also included are bases such as pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2,4,6-trime115thoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (e.g., 5-methylcytidine), 5-alkyluridines (e.g., ribothymidine), 5-halouridine (e.g., 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (e.g. 6-methyluridine), propyne, quenosine, 2-thiouridine, 4-thiouridine, wybutoxine, wybutoxosine, 4-acetylthidine, 5-(carboxyhydroxymethyl)uridine, 5"-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluridine, β-D-galactosylqueosine, 1-methyladenosine, 1-methylinosine, 2,2-dimethylguanosine, 3-methylcytidine, 2-methyladenosine, 2-methylguanosine, N6-methyladenosine, 7-methylguanosine, 5-methoxyaminomethyl-2-thiouridine, 5-methylaminomethyluridine, 5-methylcarbonylmethyluridine, 5-methoxyuridine, 5-methyl-2-thiouridine, 2-methylthio-N6-isopentenyladenosine, β-D-mannosylqueosine, uridine-5-oxyacetic acid, 2-thiocytidine, threonine derivatives and others (Burgin et al., 1996, Biochemistry, 35, 14090; Uhlman & Peyman, supra). By “modified bases” in this aspect is meant nucleotide bases other than adenine (A), guanine (G), cytosine (C), thymine (T), and uracil (U), as illustrated above; such bases can be used at any position in the antisense molecule. Persons skilled in the art will appreciate that depending on the uses of the oligomers, Ts and Us are interchangeable. For instance, with other antisense chemistries such as 2'-O-methyl antisense oligonucleotides that are more RNA-like, the T bases may be shown as U (see, e.g., Sequence ID Listing).

[0099] An “amino acid subunit” or “amino acid residue” can refer to an α-amino acid residue (e.g., —CO—CHR—NH—) or a β- or other amino acid residue (e.g., —CO—(CH₂)_nCHR—NH—), where R is a side chain (which may include hydrogen) and n is 1 to 6, preferably 1 to 4.

[0100] The term “naturally occurring amino acid” refers to an amino acid present in proteins found in nature, such as the 20 (L)-amino acids utilized during protein biosynthesis as well as others such as 4-hydroxyproline, hydroxylysine, desmosine, isodesmosine, homocysteine, citrulline and ornithine. The term “non-natural amino acids” refers to those amino acids not present in proteins found in nature, examples include beta-alanine (β-Ala; or B), 6-aminohexanoic acid (Ahx) and 6-aminopentanoic acid. Additional examples of “non-natural amino acids” include, without limitation, (D)-amino acids, norleucine, norvaline, p-fluorophenylalanine, ethionine and the like, which are known to a person skilled in the art.

[0101] An “effective amount” or “therapeutically effective amount” refers to an amount of therapeutic compound, such as an antisense oligomer, administered to a mammalian subject, either as a single dose or as part of a series of doses, which is effective to produce a desired physiological response

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or therapeutic effect in the subject. One example of a desired physiological response includes increased expression of a relatively functional or biologically active form of the dystrophin protein, mainly in muscle tissues or cells that contain a defective dystrophin protein or no dystrophin, as compared to no antisense oligomer or a control oligomer. Examples of desired therapeutic effects include, without limitation, improvements in the symptoms or pathology of muscular dystrophy, reducing the progression of symptoms or pathology of muscular dystrophy, and slowing the onset of symptoms or pathology of muscular dystrophy, among others. Examples of such symptoms include fatigue, mental retardation, muscle weakness, difficulty with motor skills (e.g., running, hopping, jumping), frequent falls, and difficulty walking. The pathology of muscular dystrophy can be characterized, for example, by muscle fibre damage and membrane leakage. For an antisense oligomer, this effect is typically brought about by altering the splice-processing of a selected target sequence (e.g., dystrophin), such as to induce exon skipping.

[0102] An "exon" refers to a defined section of nucleic acid that encodes for a protein, or a nucleic acid sequence that is represented in the mature form of an RNA molecule after either portions of a pre-processed (or precursor) RNA have been removed by splicing. The mature RNA molecule can be a messenger RNA (mRNA) or a functional form of a non-coding RNA, such as rRNA or tRNA. The human dystrophin gene has about 75 exons.

[0103] An "intron" refers to a nucleic acid region (within a gene) that is not translated into a protein. An intron is a non-coding section that is transcribed into a precursor mRNA (pre-mRNA), and subsequently removed by splicing during formation of the mature RNA.

[0104] "Exon skipping" refers generally to the process by which an entire exon, or a portion thereof, is removed from a given pre-processed RNA, and is thereby excluded from being present in the mature RNA, such as the mature mRNA that is translated into a protein. Hence, the portion of the protein that is otherwise encoded by the skipped exon is not present in the expressed form of the protein, typically creating an altered, though still functional, form of the protein. In certain embodiments, the exon being skipped is an aberrant exon from the human dystrophin gene, which may contain a mutation or other alteration in its sequence that otherwise causes aberrant splicing. In certain embodiments, the exon being skipped is any one or more of exons 1-75 of the dystrophin gene, though any one or more of exons 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, and/or 55 of the human dystrophin gene are preferred.

[0105] "Dystrophin" is a rod-shaped cytoplasmic protein, and a vital part of the protein complex that connects the cytoskeleton of a muscle fiber to the surrounding extracellular matrix through the cell membrane. Dystrophin contains multiple functional domains. For instance, dystrophin contains an actin binding domain at about amino acids 14-240 and a central rod domain at about amino acids 253-3040. This large central domain is formed by 24 spectrin-like triple-helical elements of about 109 amino acids, which have homology to alpha-actinin and spectrin. The repeats are typically interrupted by four proline-rich non-repeat segments, also referred to as hinge regions. Repeats 15 and 16 are separated by an 18 amino acid stretch that appears to provide a major site for proteolytic cleavage of dystrophin. The sequence identity between most repeats ranges from 10-25%. One repeat con-

tains three alpha-helices: 1, 2 and 3. Alpha-helices 1 and 3 are each formed by 7 helix turns, probably interacting as a coiled-coil through a hydrophobic interface. Alpha-helix 2 has a more complex structure and is formed by segments of four and three helix turns, separated by a Glycine or Proline residue. Each repeat is encoded by two exons, typically interrupted by an intron between amino acids 47 and 48 in the first part of alpha-helix 2. The other intron is found at different positions in the repeat, usually scattered over helix-3. Dystrophin also contains a cysteine-rich domain at about amino acids 3080-3360, including a cysteine-rich segment (i.e., 15 Cysteines in 280 amino acids) showing homology to the C-terminal domain of the slime mold (*Dictyostelium discoideum*) alpha-actinin. The carboxy-terminal domain is at about amino acids 3361-3685.

[0106] The amino-terminus of dystrophin binds to F-actin and the carboxy-terminus binds to the dystrophin-associated protein complex (DAPC) at the sarcolemma. The DAPC includes the dystroglycans, sarcoglycans, integrins and caveolin, and mutations in any of these components cause autosomally inherited muscular dystrophies. The DAPC is destabilized when dystrophin is absent, which results in diminished levels of the member proteins, and in turn leads to progressive fibre damage and membrane leakage. In various forms of muscular dystrophy, such as Duchenne's muscular dystrophy (DMD) and Becker's muscular dystrophy (BMD), muscle cells produce an altered and functionally defective form of dystrophin, or no dystrophin at all, mainly due to mutations in the gene sequence that lead to incorrect splicing. The predominant expression of the defective dystrophin protein, or the complete lack of dystrophin or a dystrophin-like protein, leads to rapid progression of muscle degeneration, as noted above. In this regard, a "defective" dystrophin protein may be characterized by the forms of dystrophin that are produced in certain subjects with DMD or BMD, as known in the art, or by the absence of detectable dystrophin.

[0107] Table A provides an illustration of the various dystrophin domains, the amino acid residues that encompass these domains, and the exons that encode them.

TABLE A

Domain	Sub Domain	Residue Nos	Exons
actin binding domain		14-240	2-8
central rod domain		253-3040	8-61
	hinge 1	253-327	(8)-9
	repeat 1	337-447	10-11
	repeat 2	448-556	12-14
	repeat 3	557-667	14-16
	hinge 2	668-717	17
	repeat 4	718-828	(17)-20
	repeat 5	829-934	20-21
	repeat 6	935-1045	22-23
	repeat 7	1046-1154	(23)-(26)
	repeat 8	1155-1263	26-27
	repeat 9	1264-1367	28-(30)
	repeat 10	1368-1463	30-32
	repeat 11	1464-1568	32-(34)
	repeat 12	1569-1676	34-35
	repeat 13	1677-1778	36-37
	repeat 14	1779-1874	38-(40)
	repeat 15	1875-1973	40-41
	interruption	1974-1991	42
	repeat 16	1992-2101	42-43
	repeat 17	2102-2208	44-45

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TABLE A-continued

Domain	Sub Domain	Residue Nos	Exons
Cysteine-rich domain	repeat 18	2209-2318	46-48
	repeat 19	2319-2423	48-50
	hinge 3	2424-2470	50-51
	repeat 20	2471-2577	51-53
	repeat 21	2578-2686	53-(55)
	repeat 22	2687-2802	55-(57)
	repeat 23	2803-2931	57-59
	repeat 24	2932-3040	59-(61)
	hinge 4	3041-3112	61-64
		3080-3360	63-69
Carboxy-terminal domain	dystroglycan binding site	3080-3408	63-70
	WW domain	3056-3092	62-63
	EF-hand 1	3130-3157	65
	EF-hand 2	3178-3206	65-66
	ZZ domain	3307-3354	68-69
		3361-3685	70-79
	alpha1-syntrophin binding site	3444-3494	73-74
	β1-syntrophin binding site	3495-3535	74-75
	(Leu)6-heptad repeat	3558-3593	75

[0108] As used herein, the terms "function" and "functional" and the like refer to a biological, enzymatic, or therapeutic function.

[0109] A "functional" dystrophin protein refers generally to a dystrophin protein having sufficient biological activity to reduce the progressive degradation of muscle tissue that is otherwise characteristic of muscular dystrophy, typically as compared to the altered or "defective" form of dystrophin protein that is present in certain subjects with DMD or BMD. In certain embodiments, a functional dystrophin protein may have about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% (including all integers in between) of the in vitro or in vivo biological activity of wild-type dystrophin, as measured according to routine techniques in the art. As one example, dystrophin-related activity in muscle cultures in vitro can be measured according to myotube size, myofibril organization (or disorganization), contractile activity, and spontaneous clustering of acetylcholine receptors (see, e.g., Brown et al., *Journal of Cell Science*. 112:209-216, 1999). Animal models are also valuable resources for studying the pathogenesis of disease, and provide a means to test dystrophin-related activity. Two of the most widely used animal models for DMD research are the mdx mouse and the golden retriever muscular dystrophy (GRMD) dog, both of which are dystrophin negative (see, e.g., Collins & Morgan, *Int J Exp Pathol* 84: 165-172, 2003). These and other animal models can be used to measure the functional activity of various dystrophin proteins. Included are truncated forms of dystrophin, such as those forms that are produced by certain of the exon-skipping antisense compounds of the present invention.

[0110] By "gene" is meant a unit of inheritance that occupies a specific locus on a chromosome and consists of transcriptional and/or translational regulatory sequences and/or a coding region and/or non-translated sequences (i.e., introns, 5' and 3' untranslated sequences).

[0111] By "isolated" is meant material that is substantially or essentially free from components that normally accompany it in its native state. For example, an "isolated polynucleotide," as used herein, may refer to a polynucleotide that has been purified or removed from the sequences that flank it in a

naturally-occurring state, e.g., a DNA fragment that has been removed from the sequences that are normally adjacent to the fragment.

[0112] By "enhance" or "enhancing," or "increase" or "increasing," or "stimulate" or "stimulating," refers generally to the ability of one or antisense compounds or compositions to produce or cause a greater physiological response (i.e., downstream effects) in a cell or a subject, as compared to the response caused by either no antisense compound or a control compound. A measurable physiological response may include increased expression of a functional form of a dystrophin protein, or increased dystrophin-related biological activity in muscle tissue, among other responses apparent from the understanding in the art and the description herein. Increased muscle function can also be measured, including increases or improvements in muscle function by about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100%. The percentage of muscle fibres that express a functional dystrophin can also be measured, including increased dystrophin expression in about 1%, 2%, %, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of muscle fibres. For instance, it has been shown that around 40% of muscle function improvement can occur if 25-30% of fibers express dystrophin (see, e.g., Dellor Russo et al, *Proc Natl Acad Sci USA* 99: 12979-12984, 2002). An "increased" or "enhanced" amount is typically a "statistically significant" amount, and may include an increase that is 1.1, 1.2, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50 or more times (e.g., 500, 1000 times) (including all integers and decimal points in between and above 1), e.g., 1.5, 1.6, 1.7, 1.8, etc.) the amount produced by no antisense compound (the absence of an agent) or a control compound.

[0113] The term "reduce" or "inhibit" may relate generally to the ability of one or more antisense compounds of the invention to "decrease" a relevant physiological or cellular response, such as a symptom of a disease or condition described herein, as measured according to routine techniques in the diagnostic art. Relevant physiological or cellular responses (in vivo or in vitro) will be apparent to persons skilled in the art, and may include reductions in the symptoms or pathology of muscular dystrophy, or reductions in the expression of defective forms of dystrophin, such as the altered forms of dystrophin that are expressed in individuals with DMD or BMD. A "decrease" in a response may be statistically significant as compared to the response produced by no antisense compound or a control composition, and may include a 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% decrease, including all integers in between.

[0114] "Homology" refers to the percentage number of amino acids that are identical or constitute conservative substitutions. Homology may be determined using sequence comparison programs such as GAP (Devereux et al., 1984, *Nucleic Acids Research* 12, 387-395). In this way sequences of a similar or substantially different length to those cited herein could be compared by insertion of gaps into the alignment, such gaps being determined, for example, by the comparison algorithm used by GAP.

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[0115] The recitations “sequence identity” or, for example, comprising a “sequence 50% identical to,” as used herein, refer to the extent that sequences are identical on a nucleotide-by-nucleotide basis or an amino acid-by-amino acid basis over a window of comparison. Thus, a “percentage of sequence identity” may be calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, I) or the identical amino acid residue (e.g., Ala, Pro, Ser, Thr, Gly, Val, Leu, Ile, Phe, Tyr, Trp, Lys, Arg, His, Asp, Glu, Asn, Gln, Cys and Met) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity.

[0116] Terms used to describe sequence relationships between two or more polynucleotides or polypeptides include “reference sequence,” “comparison window,” “sequence identity,” “percentage of sequence identity,” and “substantial identity”. A “reference sequence” is at least 8 or 10 but frequently 15 to 18 and often at least 25 monomer units, inclusive of nucleotides and amino acid residues, in length. Because two polynucleotides may each comprise (1) a sequence (i.e., only a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a “comparison window” to identify and compare local regions of sequence similarity. A “comparison window” refers to a conceptual segment of at least 6 contiguous positions, usually about 50 to about 100, more usually about 100 to about 150 in which a sequence is compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. The comparison window may comprise additions or deletions (i.e., gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by computerized implementations of algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, Wis., USA) or by inspection and the best alignment (i.e., resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be made to the BLAST family of programs as for example disclosed by Altschul et al., 1997, *Nucl. Acids Res.* 25:3389. A detailed discussion of sequence analysis can be found in Unit 19.3 of Ausubel et al., “Current Protocols in Molecular Biology,” John Wiley & Sons Inc, 1994-1998, Chapter 15.

[0117] “Treatment” or “treating” of an individual (e.g., a mammal, such as a human) or a cell may include any type of intervention used in an attempt to alter the natural course of the individual or cell. Treatment includes, but is not limited to, administration of a pharmaceutical composition, and may be performed either prophylactically or subsequent to the initiation of a pathologic event or contact with an etiologic agent. Treatment includes any desirable effect on the symptoms or pathology of a disease or condition associated with the dystrophin protein, as in certain forms of muscular dystrophy,

and may include, for example, minimal changes or improvements in one or more measurable markers of the disease or condition being treated. Also included are “prophylactic” treatments, which can be directed to reducing the rate of progression of the disease or condition being treated, delaying the onset of that disease or condition, or reducing the severity of its onset. “Treatment” or “prophylaxis” does not necessarily indicate complete eradication, cure, or prevention of the disease or condition, or associated symptoms thereof.

[0118] Hence, included are methods of treating muscular dystrophy, such as DMD and BMD, by administering one or more antisense oligomers of the present invention (e.g., SEQ ID NOS: 1 to 569 and 612 to 635, and variants thereof), optionally as part of a pharmaceutical formulation or dosage form, to a subject in need thereof. Also included are methods of inducing exon-skipping in a subject by administering one or more antisense oligomers, in which the exon is one of exons 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, and/or 55 from the dystrophin gene, preferably the human dystrophin gene. A “subject,” as used herein, includes any animal that exhibits a symptom, or is at risk for exhibiting a symptom, which can be treated with an antisense compound of the invention, such as a subject that has or is at risk for having DMD or BMD, or any of the symptoms associated with these conditions (e.g., muscle fibre loss). Suitable subjects (patients) include laboratory animals (such as mouse, rat, rabbit, or guinea pig), farm animals, and domestic animals or pets (such as a cat or dog). Non-human primates and, preferably, human patients, are included.

[0119] Also included are vector delivery systems that are capable of expressing the oligomeric, dystrophin-targeting sequences of the present invention, such as vectors that express a polynucleotide sequence comprising any one or more of SEQ ID NOS: 1 to 569 and 612 to 635, or variants thereof, as described herein. By “vector” or “nucleic acid construct” is meant a polynucleotide molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, yeast or virus, into which a polynucleotide can be inserted or cloned. A vector preferably contains one or more unique restriction sites and can be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integrable with the genome of the defined host such that the cloned sequence is reproducible. Accordingly, the vector can be an autonomously replicating vector, i.e., a vector that exists as an extra-chromosomal entity, the replication of which is independent of chromosomal replication, e.g., a linear or closed circular plasmid, an extra-chromosomal element, a mini-chromosome, or an artificial chromosome. The vector can contain any means for assuring self-replication. Alternatively, the vector can be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated.

[0120] A vector or nucleic acid construct system can comprise a single vector or plasmid, two or more vectors or plasmids, which together contain the total DNA to be introduced into the genome of the host cell, or a transposon. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. In the present case, the vector or nucleic acid construct is preferably one which is operably functional in a mammalian cell, such as a muscle cell. The vector can also include a selection marker such as an antibiotic or drug resistance gene, or a reporter gene (i.e., green fluorescent protein,

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luciferase), that can be used for selection or identification of suitable transformants or transfectants. Exemplary delivery systems may include viral vector systems (i.e., viral-mediated transduction) including, but not limited to, retroviral (e.g., lentiviral) vectors, adenoviral vectors, adeno-associated viral vectors, and herpes viral vectors, among others known in the art.

[0121] The term “operably linked” as used herein means placing an oligomer-encoding sequence under the regulatory control of a promoter, which then controls the transcription of the oligomer.

[0122] A wild-type gene or gene product is that which is most frequently observed in a population and is thus arbitrarily designed the “normal” or “wild-type” form of the gene.

[0123] “Alkyl” or “alkylene” both refer to a saturated straight or branched chain hydrocarbon radical containing from 1 to 18 carbons. Examples include without limitation methyl, ethyl, propyl, iso-propyl, butyl, iso-butyl, tert-butyl, n-pentyl and n-hexyl. The term “lower alkyl” refers to an alkyl group, as defined herein, containing between 1 and 8 carbons.

[0124] “Alkenyl” refers to an unsaturated straight or branched chain hydrocarbon radical containing from 2 to 18 carbons and comprising at least one carbon to carbon double bond. Examples include without limitation ethenyl, propenyl, iso-propenyl, butenyl, iso-butenyl, tert-butenyl, n-pentenyl and n-hexenyl. The term “lower alkenyl” refers to an alkenyl group, as defined herein, containing between 2 and 8 carbons.

[0125] “Alkynyl” refers to an unsaturated straight or branched chain hydrocarbon radical containing from 2 to 18 carbons comprising at least one carbon to carbon triple bond. Examples include without limitation ethynyl, propynyl, iso-propynyl, butynyl, iso-butyynyl, tert-butyynyl, pentynyl and hexynyl. The term “lower alkynyl” refers to an alkynyl group, as defined herein, containing between 2 and 8 carbons.

[0126] “Cycloalkyl” refers to a mono- or poly-cyclic alkyl radical. Examples include without limitation cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctyl.

[0127] “Aryl” refers to a cyclic aromatic hydrocarbon moiety containing from 10 to 18 carbons having one or more closed ring(s). Examples include without limitation phenyl, benzyl, naphthyl, anthracenyl, phenanthracenyl and biphenyl.

[0128] “Aralkyl” refers to a radical of the formula RaRb where Ra is an alkylene chain as defined above and Rb is one or more aryl radicals as defined above, for example, benzyl, diphenylmethyl and the like.

[0129] “Thioalkoxy” refers to a radical of the formula —SRc where Rc is an alkyl radical as defined herein. The term “lower thioalkoxy” refers to an alkoxy group, as defined herein, containing between 1 and 8 carbons.

[0130] “Alkoxy” refers to a radical of the formula —ORd where Rd is an alkyl radical as defined herein. The term “lower alkoxy” refers to an alkoxy group, as defined herein, containing between 1 and 8 carbons. Examples of alkoxy groups include, without limitation, methoxy and ethoxy.

[0131] “Alkoxyalkyl” refers to an alkyl group substituted with an alkoxy group.

[0132] “Carbonyl” refers to the C(=O)— radical.

[0133] “Guanidinyl” refers to the H₂N(C=NH₂)—NH— radical.

[0134] “Amidinyl” refers to the H₂N(C=NH₂)CH— radical.

[0135] “Amino” refers to the NH₂ radical.

[0136] “Alkylamino” refers to a radical of the formula —NHRd or —NRdRd where each Rd is, independently, an alkyl radical as defined herein. The term “lower alkylamino” refers to an alkylamino group, as defined herein, containing between 1 and 8 carbons.

[0137] “Heterocycle” means a 5- to 7-membered monocyclic, or 7- to 10-membered bicyclic, heterocyclic ring which is either saturated, unsaturated, or aromatic, and which contains from 1 to 4 heteroatoms independently selected from nitrogen, oxygen and sulfur, and wherein the nitrogen and sulfur heteroatoms may be optionally oxidized, and the nitrogen heteroatom may be optionally quaternized, including bicyclic rings in which any of the above heterocycles are fused to a benzene ring. The heterocycle may be attached via any heteroatom or carbon atom. Heterocycles include heteroaryls as defined below. Thus, in addition to the heteroaryls listed below, heterocycles also include morpholinyl, pyrrolidinyl, pyrrolidinyl, piperidinyl, piperizinyl, hydantoinyl, valerolactamyl, oxiranyl, oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, tetrahydropyridinyl, tetrahydrothiophenyl, tetrahydrothiopyranyl, tetrahydropyrimidinyl, tetrahydrothiopyranyl, and the like.

[0138] “Heteroaryl” means an aromatic heterocycle ring of 5- to 10 members and having at least one heteroatom selected from nitrogen, oxygen and sulfur, and containing at least 1 carbon atom, including both mono- and bicyclic ring systems. Representative heteroaryls are pyridyl, furyl, benzofuranyl, thiophenyl, benzothiophenyl, quinolinyl, pyrrolyl, indolyl, oxazolyl, benzoxazolyl, imidazolyl, benzimidazolyl, thiazolyl, benzothiazolyl, isoxazolyl, pyrazolyl, isothiazolyl, pyridazinyl, pyrimidinyl, pyrazinyl, triazinyl, cinnolinyl, phthalazinyl, and quinazolinyl.

[0139] The terms “optionally substituted alkyl”, “optionally substituted alkenyl”, “optionally substituted alkoxy”, “optionally substituted thioalkoxy”, “optionally substituted alkyl amino”, “optionally substituted lower alkyl”, “optionally substituted lower alkenyl”, “optionally substituted lower alkoxy”, “optionally substituted lower thioalkoxy”, “optionally substituted lower alkyl amino” and “optionally substituted heterocycle” mean that, when substituted, at least one hydrogen atom is replaced with a substituent. In the case of an oxo substituent (=O) two hydrogen atoms are replaced. In this regard, substituents include: deuterium, optionally substituted alkyl, optionally substituted alkenyl, optionally substituted alkynyl, optionally substituted aryl, optionally substituted heterocycle, optionally substituted cycloalkyl, o xo, halogen, —CN, —ORx, NRxRy, NRxC(=O)Ry, NRxSO2Ry, NRxC(=O)NRxRy, C(=O)Rx, C(=O)ORx, C(=O)NRxRy, —SOMRx and —SOMNRxRy, wherein m is 0, 1 or 2, Rx and Ry are the same or different and independently hydrogen, optionally substituted alkyl, optionally substituted alkenyl, optionally substituted alkynyl, optionally substituted aryl, optionally substituted heterocycle or optionally substituted cycloalkyl and each of said optionally substituted alkyl, optionally substituted alkenyl, optionally substituted alkynyl, optionally substituted aryl, optionally substituted heterocycle and optionally substituted cycloalkyl substituents may be further substituted with one or more of oxo, halogen, —CN, —ORx, NRxRy, NRxC(=O)Ry, NRxSO2Ry, —NRxC(=O)NRxRy, C(=O)Rx, C(=O)ORx, C(=O)NRxRy, —SOMRx and —SOMNRxRy.

Constructing Antisense Oligonucleotides

[0140] Examples of morpholino oligonucleotides having phosphorus-containing backbone linkages are illustrated in

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FIGS. 1A-1C. Especially preferred is a phosphorodiamidate-linked morpholino oligonucleotide such as shown in FIG. 1C, which is modified, in accordance with one aspect of the present invention, to contain positively charged groups at preferably 10%-50% of its backbone linkages. Morpholino oligonucleotides with uncharged backbone linkages and their preparation, including antisense oligonucleotides, are detailed, for example, in (Summerton and Weller 1997) and in co-owned U.S. Pat. Nos. 5,698,685, 5,217,866, 5,142,047, 5,034,506, 5,166,315, 5,185,444, 5,521,063, and 5,506,337, all of which are expressly incorporated by reference herein.

[0141] Important properties of the morpholino-based subunits include: 1) the ability to be linked in a oligomeric form by stable, uncharged or positively charged backbone linkages; 2) the ability to support a nucleotide base (e.g. adenine, cytosine, guanine, thymidine, uracil and inosine) such that the polymer formed can hybridize with a complementary-base target nucleic acid, including target RNA, T_m values above about 45° C. in relatively short oligonucleotides (e.g., 10-15 bases); 3) the ability of the oligonucleotide to be actively or passively transported into mammalian cells; and 4) the ability of the antisense oligonucleotide:RNA heteroduplex to resist RNase and RNaseH degradation, respectively.

[0142] Exemplary backbone structures for antisense oligonucleotides of the claimed subject matter include the morpholino subunit types shown in FIGS. 1D-G, each linked by an uncharged or positively charged, phosphorus-containing subunit linkage. FIG. 1D shows a phosphorus-containing linkage which forms the five atom repeating-unit backbone, wherein the morpholino rings are linked by a 1-atom phosphoamide linkage. FIG. 1E shows a linkage which produces a 6-atom repeating-unit backbone. In this structure, the atom Y linking the 5' morpholino carbon to the phosphorus group may be sulfur, nitrogen, carbon or, preferably, oxygen. The X moiety pendant from the phosphorus may be fluorine, an alkyl or substituted alkyl, an alkoxy or substituted alkoxy, a thioalkoxy or substituted thioalkoxy, or unsubstituted, mono-substituted, or disubstituted nitrogen, including cyclic structures, such as morpholines or piperidines. Alkyl, alkoxy and thioalkoxy preferably include 1-6 carbon atoms. The Z moieties are sulfur or oxygen, and are preferably oxygen.

[0143] The linkages shown in FIGS. 1F and 1G are designed for 7-atom unit-length backbones. In structure 1F, the X moiety is as in Structure 1E, and the Y moiety may be methylene, sulfur, or, preferably, oxygen. In Structure 1G, the X and Y moieties are as in Structure 1E. Particularly preferred morpholino oligonucleotides include those composed of morpholino subunit structures of the form shown in FIG. 1E, where X=NH₂, N(CH₃)₂, optionally substituted 1-piperazinyl, or other charged group, Y=O, and Z=O.

[0144] As noted above, the uncharged or substantially uncharged oligonucleotide may be modified, in accordance with an aspect of the invention, to include charged linkages, e.g. up to about 1 per every 2-5 uncharged linkages, such as about 4-5 per every 10 uncharged linkages. Optimal improvement in antisense activity may be seen when about 25% of the backbone linkages are cationic, including about 20% to about 30%. Also included are oligomers in which about 35%, 40%, 45%, 50%, 55%, 60% (including all integers in between), or more of the backbone linkages are cationic. Enhancement is also seen with a small number, e.g., 5% or 10-20%, of cationic linkages.

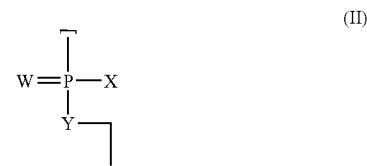
[0145] A substantially uncharged, phosphorus containing backbone in an oligonucleotide analog is typically one in

which a majority of the subunit linkages, e.g., between 50%-100%, typically at least 60% to 100% or 75% or 80% of its linkages, are uncharged at physiological pH and contain a single phosphorous atom.

[0146] Additional experiments conducted in support of the present invention indicate that the enhancement seen with added cationic backbone charges may, in some cases, be further enhanced by distributing the bulk of the charges close to the "center-region" backbone linkages of the antisense oligonucleotide, e.g., in a 20mer oligonucleotide with 8 cationic backbone linkages, having at least 70% of these charged linkages localized in the 10 centermost linkages.

[0147] The antisense compounds can be prepared by step-wise solid-phase synthesis, employing methods detailed in the references cited above, and below with respect to the synthesis of oligonucleotides having a mixture of uncharged and cationic backbone linkages. In some cases, it may be desirable to add additional chemical moieties to the antisense compound, e.g. to enhance pharmacokinetics or to facilitate capture or detection of the compound. Such a moiety may be covalently attached, typically to a terminus of the oligomer, according to standard synthetic methods. For example, addition of a polyethyleneglycol moiety or other hydrophilic polymer, e.g., one having 10-100 monomeric subunits, may be useful in enhancing solubility. One or more charged groups, e.g., anionic charged groups such as an organic acid, may enhance cell uptake. A reporter moiety, such as fluorescein or a radiolabeled group, may be attached for purposes of detection. Alternatively, the reporter label attached to the oligomer may be a ligand, such as an antigen or biotin, capable of binding a labeled antibody or streptavidin. In selecting a moiety for attachment or modification of an antisense compound, it is generally of course desirable to select chemical compounds of groups that are biocompatible and likely to be tolerated by a subject without undesirable side effects.

[0148] As noted above, the antisense compound can be constructed to contain a selected number of cationic linkages interspersed with uncharged linkages of the type described above. The intersubunit linkages, both uncharged and cationic, preferably are phosphorus-containing linkages, having the structure (II):



wherein:

[0149] W is —S— or —O—, and is preferably —O—,

[0150] X=NR¹R² or —OR⁶,

[0151] Y=—O— or —NR⁷, and

[0152] each said linkage in the oligomer is selected from:

[0153] (a) an uncharged linkage (a), wherein each of R¹, R², R⁶ and R⁷ is independently selected from hydrogen and lower alkyl;

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[0154] (b1) a cationic linkage (b1), wherein X=—NR¹R² and Y=—O—, and —NR¹R² represents an optionally substituted piperazinyl moiety, such that R¹R²=—CHRCHRN(R³)(R⁴)CHRCHR—, wherein:

[0155] each R is independently H or —CH₃,

[0156] R⁴ is H, —CH₃, or an electron pair, and

[0157] R³ is selected from H, optionally substituted lower alkyl, —C(=NH)NH₂, —Z-L-NHC(=NH)NH₂, and [—C(=O)CHR'NH]_mH, where: Z is —C(=O)— or a direct bond, L is an optional linker up to 18 atoms in length, preferably up to 12 atoms, and more preferably up to 8 atoms in length, having bonds selected from optionally substituted alkyl, optionally substituted alkoxy, and optionally substituted alkylamino, R' is a side chain of a naturally occurring amino acid or a one- or two-carbon homolog thereof, and m is 1 to 6, preferably 1 to 4;

[0158] (b2) a cationic linkage (b2), wherein X=—NR¹R² and Y=—O—, R¹=H or —CH₃, and R²=LNR³R⁴R⁵, wherein L, R³, and R⁴ are as defined above, and R⁵ is H, optionally substituted lower alkyl, or optionally substituted lower (alkoxy)alkyl; and

[0159] (b3) a cationic linkage (b3), wherein Y=—NR⁷ and X=—OR⁶, and R⁷=—LNR³R⁴R⁵, wherein L, R³, R⁴ and R⁵ are as defined above, and R⁶ is H or optionally substituted lower alkyl; and

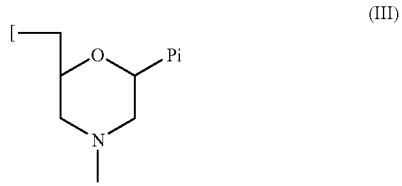
[0160] at least one said linkage is selected from cationic linkages (b1), (b2), and (b3).

[0161] Preferably, the oligomer includes at least two consecutive linkages of type (a) (i.e. uncharged linkages). In further embodiments, at least 5% of the linkages in the oligomer are cationic linkages (i.e. type (b1), (b2), or (b3)); for example, 10% to 60%, and preferably 20-50% linkages may be cationic linkages.

[0162] In one embodiment, at least one linkage is of type (b1), where, preferably, each R is H, R⁴ is H, —CH₃, or an electron pair, and R³ is selected from H, optionally substituted lower alkyl, —C(=NH)NH₂, and —C(=O)-L-NHC(=NH)NH₂. The latter two embodiments of R³ provide a guanidino moiety, either attached directly to the piperazine ring, or pendant to a linker group L, respectively. For ease of synthesis, the variable Z in R³ is preferably —C(=O)—, as shown.

[0163] The linker group L, as noted above, contains bonds in its backbone selected from optionally substituted alkyl, optionally substituted alkoxy, and optionally substituted alkylamino, wherein the terminal atoms in L (e.g., those adjacent to carbonyl or nitrogen) are carbon atoms. Although branched linkages are possible, the linker is preferably unbranched. In one embodiment, the linker is a linear alkyl linker. Such a linker may have the structure —(CH₂)_n—, where n is 1-12, preferably 2-8, and more preferably 2-6.

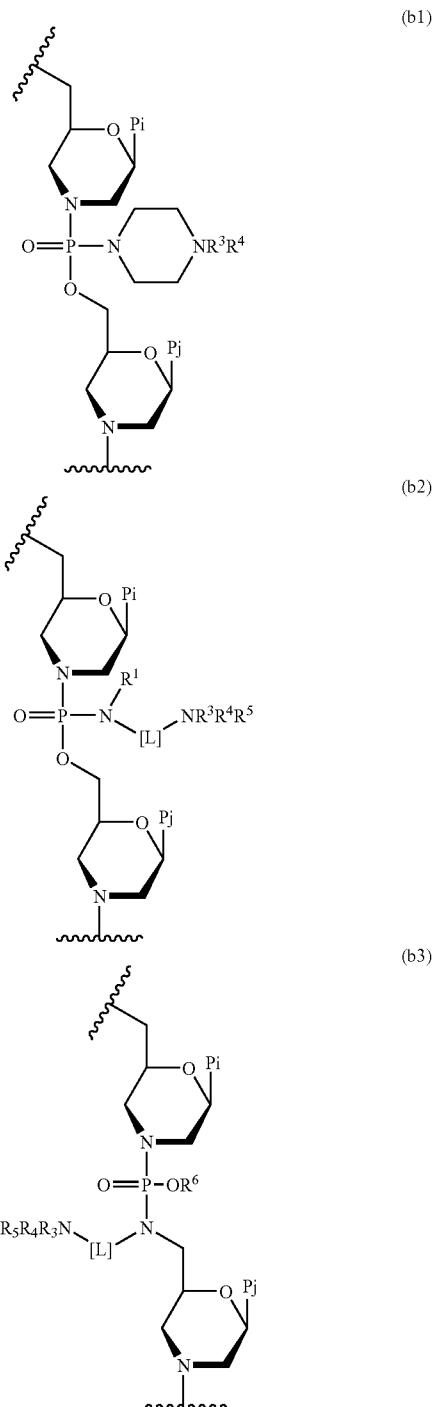
[0164] The morpholino subunits have the following structure (III):



wherein Pi is a base-pairing moiety, and the linkages depicted above connect the nitrogen atom of (III) to the 5' carbon of an

adjacent subunit. The base-pairing moieties Pi may be the same or different, and are generally designed to provide a sequence which binds to a target nucleic acid.

[0165] The use of embodiments of linkage types (b1), (b2) and (b3) above to link morpholino subunits (III) may be illustrated graphically as follows:



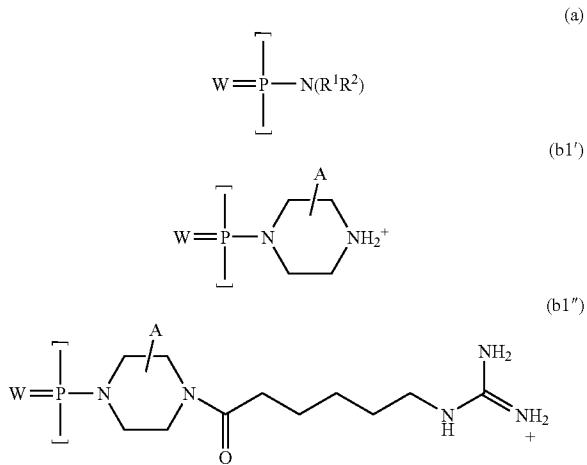
[0166] Preferably, all cationic linkages in the oligomer are of the same type; i.e. all of type (b1), all of type (b2), or all of type (b3).

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[0167] In further embodiments, the cationic linkages are selected from linkages (b1') and (b1'') as shown below, where (b1') is referred to herein as a "Pip" linkage and (b1'') is referred to herein as a "GuX" linkage:



[0168] In the structures above, W is S or O, and is preferably O; each of R¹ and R² is independently selected from hydrogen and optionally substituted lower alkyl, and is preferably methyl; and A represents hydrogen or a non-interfering substituent (i.e. a substituent that does not adversely affect the ability of an oligomer to bind to its intended target) on one or more carbon atoms in (b1') and (b1''). Preferably, the ring carbons in the piperazine ring are unsubstituted; however, the ring carbons of the piperazine ring may include non-interfering substituents, such as methyl or fluorine. Preferably, at most one or two carbon atoms is so substituted.

[0169] In further embodiments, at least 10% of the linkages are of type (b1') or (b1''); for example, 10%-60% and preferably 20% to 50%, of the linkages may be of type (b1') or (b1'').

[0170] In other embodiments, the oligomer contains no linkages of the type (b1') above. Alternatively, the oligomer contains no linkages of type (b1) where each R is H, R³ is H or —CH₃, and R⁴ is H, —CH₃, or an electron pair.

[0171] The morpholino subunits may also be linked by non-phosphorus-based intersubunit linkages, as described further below, where at least one linkage is modified with a pendant cationic group as described above.

[0172] Other oligonucleotide analog linkages which are uncharged in their unmodified state but which could also bear a pendant amine substituent could be used. For example, a 5' nitrogen atom on a morpholino ring could be employed in a sulfamide linkage or a urea linkage (where phosphorus is replaced with carbon or sulfur, respectively) and modified in a manner analogous to the 5'-nitrogen atom in structure (b3) above.

[0173] Oligomers having any number of cationic linkages are provided, including fully cationic-linked oligomers. Preferably, however, the oligomers are partially charged, having, for example, 10%-80%. In preferred embodiments, about 10% to 60%, and preferably 20% to 50% of the linkages are cationic.

[0174] In one embodiment, the cationic linkages are interspersed along the backbone. The partially charged oligomers preferably contain at least two consecutive uncharged link-

ages; that is, the oligomer preferably does not have a strictly alternating pattern along its entire length.

[0175] Also considered are oligomers having blocks of cationic linkages and blocks of uncharged linkages; for example, a central block of uncharged linkages may be flanked by blocks of cationic linkages, or vice versa. In one embodiment, the oligomer has approximately equal-length 5', 3' and center regions, and the percentage of cationic linkages in the center region is greater than about 50%, preferably greater than about 70%.

[0176] Oligomers for use in antisense applications generally range in length from about 10 to about 40 subunits, more preferably about 10 to 30 subunits, and typically 15-25 bases, including those having 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 bases. In certain embodiments, an oligomer of the invention having 19-20 subunits, a useful length for an antisense compound, may ideally have two to ten, e.g., four to eight, cationic linkages, and the remainder uncharged linkages. An oligomer having 14-15 subunits may ideally have two to seven, e.g., 3 to 5, cationic linkages, and the remainder uncharged linkages.

[0177] Each morpholino ring structure supports a base pairing moiety, to form a sequence of base pairing moieties which is typically designed to hybridize to a selected antisense target in a cell or in a subject being treated. The base pairing moiety may be a purine or pyrimidine found in native DNA or RNA (e.g., A, G, C, T or U) or an analog, such as hypoxanthine (the base component of the nucleoside inosine) or 5-methyl cytosine.

Peptide Transporters

[0178] The antisense compounds of the invention may include an oligonucleotide moiety conjugated to an arginine-rich peptide transport moiety effective to enhance transport of the compound into cells. The transport moiety is preferably attached to a terminus of the oligomer, as shown, for example, in FIGS. 1B and 1C. The peptide transport moiety preferably comprises 6 to 16 subunits selected from X' subunits, Y' subunits, and Z' subunits, wherein:

[0179] (a) each X' subunit independently represents lysine, arginine or an arginine analog, said analog being a cationic α -amino acid comprising a side chain of the structure R¹N=C(NH₂)R², where R¹ is H or R; R² is R, —NH₂, —NHR, or —NR₂, where R is optionally substituted lower alkyl or optionally substituted lower alkenyl; R¹ and R² may join together to form a ring; and the side chain is linked to said amino acid via R¹ or R²;

[0180] (b) each Y' subunit independently represents a neutral amino acid —C(=O)—(CHR)_n—NH—, where n is 2 to 7 and each R is independently H or methyl; and

[0181] (c) each Z' subunit independently represents an α -amino acid having a neutral aralkyl side chain; wherein the peptide comprises a sequence represented by at least one of (X'YX')_p, (X'Y')_m, and/or (X'Z'Z')_p, where p is 2 to 5 and m is 2 to 8. Certain embodiments include various combinations selected independently from (X'YX')_p, (X'Y')_m, and/or (X'Z'Z')_p, including, for example, peptides having the sequence (X'YX')(X'Z'Z')(X'YX')(X'Z'Z') (SEQ ID NO:637).

[0182] In selected embodiments, for each X', the side chain moiety is guanidyl, as in the amino acid subunit arginine (Arg). In certain embodiments, each Y' is independently —C(=O)—(CH₂)_n—CHR—NH—, where n is 2 to 7 and R is

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H. For example, when n is 5 and R is H, Y' is a 6-aminohexanoic acid subunit, abbreviated herein as Ahx; when n is 2 and R is H, Y' is a β-alanine subunit, abbreviated herein as B. Certain embodiments relate to carrier peptides having a combination of different neutral amino acids, including, for example, peptides comprising the sequence —RahxRRBRAhxAhxRRBRAhxB— (SEQ ID NO:578), which contains both β-alanine and 6-aminohexanoic acid.

[0183] Preferred peptides of this type include those comprising arginine dimers alternating with single Y' subunits, where Y' is preferably Ahx or B or both. Examples include peptides having the formula (RY'R)_p and/or the formula (RRY')_p, where p is 1 to 2 to 5 and where Y' is preferably Ahx. In one embodiment, Y' is a 6-aminohexanoic acid subunit, R is arginine and p is 4. Certain embodiments include various linear combinations of at least two of (RY'R)_p and (RRY')_p, including, for example, illustrative peptides having the sequence (RY'R)(RRY')(RY'R)(RRY') (SEQ ID NO:638), or (RRY')(RY'R)(RRY') (SEQ ID NO:639). Other combinations are contemplated. In a further illustrative embodiment, each Z' is phenylalanine, and m is 3 or 4.

[0184] The conjugated peptide is preferably linked to a terminus of the oligomer via a linker Ahx-B, where Ahx is a 6-aminohexanoic acid subunit and B is a β-alanine subunit, as shown, for example, in FIGS. 1B and 1C.

[0185] In selected embodiments, for each X', the side chain moiety is independently selected from the group consisting of guanidyl (HN=C(NH₂)NH—), amidinyl (HN=C(NH₂)CH—), 2-aminodihydropyrimidyl, 2-aminotetrahydropyrimidyl, 2-aminopyridinyl, and 2-aminopyrimidinyl, and it is preferably selected from guanidyl and amidinyl. In one embodiment, the side chain moiety is guanidyl, as in the amino acid subunit arginine (Arg).

[0186] In certain embodiments, the Y' subunits may be contiguous, in that no X' subunits intervene between Y' subunits, or interspersed singly between X' subunits. In certain embodiments, the linking subunit may be between Y' subunits. In one embodiment, the Y' subunits are at a terminus of the transporter; in other embodiments, they are flanked by X' subunits. In further preferred embodiments, each Y' is —C(=O)—(CH₂)_n—CHR—NH—, where n is 2 to 7 and R is H. For example, when n is 5 and R is H, Y' is a 6-aminohexanoic acid subunit, abbreviated herein as Ahx. In selected embodiments of this group, each X' comprises a guanidyl side chain moiety, as in an arginine subunit. Preferred peptides of this type include those comprising arginine dimers alternat-

ing with single Y' subunits, where Y' is preferably Ahx. Examples include peptides having the formula (RY'R)₄ or the formula (RRY')₄, where Y' is preferably Ahx. In the latter case, the nucleic acid analog is preferably linked to a terminal Y' subunit, preferably at the C-terminus, as shown, for example, in FIGS. 1B and 1C. The preferred linker is of the structure AhxB, where Ahx is a 6-aminohexanoic acid subunit and B is a β-alanine subunit.

[0187] The transport moieties as described above have been shown to greatly enhance cell entry of attached oligomers, relative to uptake of the oligomer in the absence of the attached transport moiety, and relative to uptake by an attached transport moiety lacking the hydrophobic subunits Y'. Such enhanced uptake is preferably evidenced by at least a two-fold increase, and preferably a four-fold increase, in the uptake of the compound into mammalian cells relative to uptake of the agent by an attached transport moiety lacking the hydrophobic subunits Y'. Uptake is preferably enhanced at least twenty fold, and more preferably forty fold, relative to the unconjugated compound.

[0188] A further benefit of the transport moiety is its expected ability to stabilize a duplex between an antisense compound and its target nucleic acid sequence, presumably by virtue of electrostatic interaction between the positively charged transport moiety and the negatively charged nucleic acid. The number of charged subunits in the transporter is less than 14, as noted above, and preferably between 8 and 11, since too high a number of charged subunits may lead to a reduction in sequence specificity.

[0189] The use of arginine-rich peptide transporters (i.e., cell-penetrating peptides) is particularly useful in practicing the present invention. Certain peptide transporters have been shown to be highly effective at delivery of antisense compounds into primary cells including muscle cells (Marshall, Oda et al. 2007; Jearawiriyapaisarn, Moulton et al. 2008; Wu, Moulton et al. 2008). Furthermore, compared to other peptide transporters such as Penetratin and the Tat peptide, the peptide transporters described herein, when conjugated to an antisense PMO, demonstrate an enhanced ability to alter splicing of several gene transcripts (Marshall, Oda et al. 2007). Especially preferred are the P007, CP06062 and CP04057 transport peptides listed below in Table 3 (SEQ ID NOS: 573, 578 and 577, respectively).

[0190] Exemplary peptide transporters, including linkers (B or AhxB) are given below in Table B below. Preferred sequences are those designated CP06062 (SEQ ID NO: 578), P007 (SEQ ID NO: 573) and CP04057 (SEQ ID NO: 577).

TABLE B

Exemplary Peptide Transporters for
Intracellular Delivery of PMO

Peptide	Sequence (N-terminal to C-terminal)	SEQ ID NO:
rTAT	RRRQRKKRKC	570
R ₉ F ₂	RRRRRRRRFFC	571
(RRAhxA) ₄ B	RRAhxAhxAhxAhxAhxB	572
(RAhxA) ₄ AhxR; (P007)	RAhxAhxAhxAhxAhxB	573
(AhxRR) ₄ AhxB	AhxRRAhxAhxAhxAhxB	574
(RAhxA) ₆ B	RAhxAhxAhxAhxAhxAhxB	575

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TABLE B-continued

<u>Exemplary Peptide Transporters for Intracellular Delivery of PMO</u>		<u>SEQ ID NO:</u>
<u>Peptide</u>	<u>Sequence (N-terminal to C-terminal)</u>	
(RAhx) ₈ B	RAhxRAhxRAhxRAhxRAhxRAhxRAhxRAhxB	576
(RAhxR) ₅ AhxB (CP05057)	RAhxRRAhxRRAhxRRAhxRRAhxRAhxB	577
(RAhxRRBR) ₂ AhxB; (CP06062)	RAhxRRBRRAhxRRBRAhxB	578
MSP	ASSLNIA	579

Formulations

[0191] In certain embodiments, the present invention provides formulations or compositions suitable for the therapeutic delivery of antisense oligomers, as described herein. Hence, in certain embodiments, the present invention provides pharmaceutically acceptable compositions that comprise a therapeutically-effective amount of one or more of the oligomers described herein, formulated together with one or more pharmaceutically acceptable carriers (additives) and/or diluents. While it is possible for an oligomer of the present invention to be administered alone, it is preferable to administer the compound as a pharmaceutical formulation (composition).

[0192] Methods for the delivery of nucleic acid molecules are described, for example, in Akhtar et al., 1992, *Trends Cell Bio.*, 2:139; and *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar; Sullivan et al., PCT WO 94/02595. These and other protocols can be utilized for the delivery of virtually any nucleic acid molecule, including the isolated oligomers of the present invention.

[0193] As detailed below, the pharmaceutical compositions of the present invention may be specially formulated for administration in solid or liquid form, including those adapted for the following: (1) oral administration, for example, drenches (aqueous or non-aqueous solutions or suspensions), tablets, e.g., those targeted for buccal, sublingual, and systemic absorption, boluses, powders, granules, pastes for application to the tongue; (2) parenteral administration, for example, by subcutaneous, intramuscular, intravenous or epidural injection as, for example, a sterile solution or suspension, or sustained-release formulation; (3) topical application, for example, as a cream, ointment, or a controlled-release patch or spray applied to the skin; (4) intravaginally or intrarectally, for example, as a pessary, cream or foam; (5) sublingually; (6) ocularly; (7) transdermally; or (8) nasally.

[0194] The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

[0195] The phrase "pharmaceutically-acceptable carrier" as used herein means a pharmaceutically-acceptable material, composition or vehicle, such as a liquid or solid filler,

diluent, excipient, manufacturing aid (e.g., lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in carrying or transporting the subject compound from one organ, or portion of the body, to another organ, or portion of the body. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the patient.

[0196] Some examples of materials that can serve as pharmaceutically-acceptable carriers include, without limitation: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) pH buffered solutions; (21) polyesters, polycarbonates and/or polyanhydrides; and (22) other non-toxic compatible substances employed in pharmaceutical formulations.

[0197] Additional non-limiting examples of agents suitable for formulation with the antisense oligomers of the instant invention include: PEG conjugated nucleic acids, phospholipid conjugated nucleic acids, nucleic acids containing lipophilic moieties, phosphorothioates, P-glycoprotein inhibitors (such as Pluronic P85) which can enhance entry of drugs into various tissues; biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after implantation (Emerich, D F et al., 1999, *Cell Transplant*, 8, 47-58) Alkermes, Inc. Cambridge, Mass.; and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999).

[0198] The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, branched and unbranched or combinations thereof, or long-circulating liposomes or stealth liposomes). Oligomers of the invention can also comprise covalently attached PEG molecules of various

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molecular weights. These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic et al. *Chem. Rev.* 1995, 95, 2601-2627; Ishiwata et al., *Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic et al., *Science* 1995, 267, 1275-1276; Oku et al., 1995, *Biochim. Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu et al., *J. Biol. Chem.* 1995, 42, 24864-24870; Choi et al., International PCT Publication No. WO 96/10391; Ansell et al., International PCT Publication No. WO 96/10390; Holland et al., International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

[0199] In a further embodiment, the present invention includes oligomer compositions prepared for delivery as described in U.S. Pat. Nos. 6,692,911, 7,163,695 and 7,070,807. In this regard, in one embodiment, the present invention provides an oligomer of the present invention in a composition comprising copolymers of lysine and histidine (HK) as described in U.S. Pat. Nos. 7,163,695, 7,070,807, and 6,692,911 either alone or in combination with PEG (e.g., branched or unbranched PEG or a mixture of both), in combination with PEG and a targeting moiety or any of the foregoing in combination with a crosslinking agent. In certain embodiments, the present invention provides antisense oligomers in compositions comprising gluconic-acid-modified polyhistidine or gluconylated-polyhistidine/transferrin-polylysine. One skilled in the art will also recognize that amino acids with properties similar to His and Lys may be substituted within the composition.

[0200] Certain embodiments of the oligomers described herein may contain a basic functional group, such as amino or alkylamino, and are, thus, capable of forming pharmaceutically-acceptable salts with pharmaceutically-acceptable acids. The term "pharmaceutically-acceptable salts" in this respect, refers to the relatively non-toxic, inorganic and organic acid addition salts of compounds of the present invention. These salts can be prepared in situ in the administration vehicle or the dosage form manufacturing process, or by separately reacting a purified compound of the invention in its free base form with a suitable organic or inorganic acid, and isolating the salt thus formed during subsequent purification. Representative salts include the hydrobromide, hydrochloride, sulfate, bisulfate, phosphate, nitrate, acetate, valerate, oleate, palmitate, stearate, laurate, benzoate, lactate, phosphate, tosylate, citrate, maleate, fumarate, succinate, tartrate, naphthalate, mesylate, glucoheptonate, lactobionate, and laurylsulphonate salts and the like. (See, e.g., Berge et al. (1977) "Pharmaceutical Salts", *J. Pharm. Sci.* 66:1-19).

[0201] The pharmaceutically acceptable salts of the subject oligomers include the conventional nontoxic salts or quaternary ammonium salts of the compounds, e.g., from non-toxic organic or inorganic acids. For example, such conventional

nontoxic salts include those derived from inorganic acids such as hydrochloride, hydrobromic, sulfuric, sulfamic, phosphoric, nitric, and the like; and the salts prepared from organic acids such as acetic, propionic, succinic, glycolic, stearic, lactic, malic, tartaric, citric, ascorbic, palmitic, maleic, hydroxymaleic, phenylacetic, glutamic, benzoic, salicylic, sulfanilic, 2-acetoxybenzoic, fumaric, toluene-sulfonic, methanesulfonic, ethane disulfonic, oxalic, isothionic, and the like.

[0202] In certain embodiments, the oligomers of the present invention may contain one or more acidic functional groups and, thus, are capable of forming pharmaceutically-acceptable salts with pharmaceutically-acceptable bases. The term "pharmaceutically-acceptable salts" in these instances refers to the relatively non-toxic, inorganic and organic base addition salts of compounds of the present invention. These salts can likewise be prepared in situ in the administration vehicle or the dosage form manufacturing process, or by separately reacting the purified compound in its free acid form with a suitable base, such as the hydroxide, carbonate or bicarbonate of a pharmaceutically-acceptable metal cation, with ammonia, or with a pharmaceutically-acceptable organic primary, secondary or tertiary amine. Representative alkali or alkaline earth salts include the lithium, sodium, potassium, calcium, magnesium, and aluminum salts and the like. Representative organic amines useful for the formation of base addition salts include ethylamine, diethylamine, ethylenediamine, ethanolamine, diethanolamine, piperazine and the like. (See, e.g., Berge et al., *supra*).

[0203] Wetting agents, emulsifiers and lubricants, such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, release agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the compositions.

[0204] Examples of pharmaceutically-acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[0205] Formulations of the present invention include those suitable for oral, nasal, topical (including buccal and sublingual), rectal, vaginal and/or parenteral administration. The formulations may conveniently be presented in unit dosage form and may be prepared by any methods well known in the art of pharmacy. The amount of active ingredient that can be combined with a carrier material to produce a single dosage form will vary depending upon the host being treated, the particular mode of administration. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will generally be that amount of the compound which produces a therapeutic effect. Generally, out of one hundred percent, this amount will range from about 0.1 percent to about ninety-nine percent of active ingredient, preferably from about 5 percent to about 70 percent, most preferably from about 10 percent to about 30 percent.

[0206] In certain embodiments, a formulation of the present invention comprises an excipient selected from cyclodextrins, celluloses, liposomes, micelle forming agents, e.g., bile acids, and polymeric carriers, e.g., polyesters and poly-

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anhydrides; and an oligomer of the present invention. In certain embodiments, an aforementioned formulation renders orally bioavailable an oligomer of the present invention.

[0207] Methods of preparing these formulations or compositions include the step of bringing into association an oligomer of the present invention with the carrier and, optionally, one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association a compound of the present invention with liquid carriers, or finely divided solid carriers, or both, and then, if necessary, shaping the product.

[0208] Formulations of the invention suitable for oral administration may be in the form of capsules, cachets, pills, tablets, lozenges (using a flavored basis, usually sucrose and acacia or tragacanth), powders, granules, or as a solution or a suspension in an aqueous or non-aqueous liquid, or as an oil-in-water or water-in-oil liquid emulsion, or as an elixir or syrup, or as pastilles (using an inert base, such as gelatin and glycerin, or sucrose and acacia) and/or as mouth washes and the like, each containing a predetermined amount of a compound of the present invention as an active ingredient. An oligomer of the present invention may also be administered as a bolus, electuary or paste.

[0209] In solid dosage forms of the invention for oral administration (capsules, tablets, pills, dragees, powders, granules, trouches and the like), the active ingredient may be mixed with one or more pharmaceutically-acceptable carriers, such as sodium citrate or dicalcium phosphate, and/or any of the following: (1) fillers or extenders, such as starches, lactose, sucrose, glucose, mannitol, and/or silicic acid; (2) binders, such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinyl pyrrolidone, sucrose and/or acacia; (3) humectants, such as glycerol; (4) disintegrating agents, such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate; (5) solution retarding agents, such as paraffin; (6) absorption accelerators, such as quaternary ammonium compounds and surfactants, such as poloxamer and sodium lauryl sulfate; (7) wetting agents, such as, for example, cetyl alcohol, glycerol monostearate, and non-ionic surfactants; (8) absorbents, such as kaolin and bentonite clay; (9) lubricants, such as talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, zinc stearate, sodium stearate, stearic acid, and mixtures thereof; (10) coloring agents; and (11) controlled release agents such as crospovidone or ethyl cellulose. In the case of capsules, tablets and pills, the pharmaceutical compositions may also comprise buffering agents. Solid compositions of a similar type may also be employed as fillers in soft and hard-shelled gelatin capsules using such excipients as lactose or milk sugars, as well as high molecular weight polyethylene glycols and the like.

[0210] A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared using binder (e.g., gelatin or hydroxypropylmethyl cellulose), lubricant, inert diluent, preservative, disintegrant (for example, sodium starch glycolate or cross-linked sodium carboxymethyl cellulose), surface-active or dispersing agent. Molded tablets may be made by molding in a suitable machine a mixture of the powdered compound moistened with an inert liquid diluent.

[0211] The tablets, and other solid dosage forms of the pharmaceutical compositions of the present invention, such as dragees, capsules, pills and granules, may optionally be scored or prepared with coatings and shells, such as enteric

coatings and other coatings well known in the pharmaceutical-formulating art. They may also be formulated so as to provide slow or controlled release of the active ingredient therein using, for example, hydroxypropylmethyl cellulose in varying proportions to provide the desired release profile, other polymer matrices, liposomes and/or microspheres. They may be formulated for rapid release, e.g., freeze-dried. They may be sterilized by, for example, filtration through a bacteria-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved in sterile water, or some other sterile injectable medium immediately before use. These compositions may also optionally contain opacifying agents and may be of a composition that they release the active ingredient(s) only, or preferentially, in a certain portion of the gastrointestinal tract, optionally, in a delayed manner. Examples of embedding compositions which can be used include polymeric substances and waxes. The active ingredient can also be in micro-encapsulated form, if appropriate, with one or more of the above-described excipients.

[0212] Liquid dosage forms for oral administration of the compounds of the invention include pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups and elixirs. In addition to the active ingredient, the liquid dosage forms may contain inert diluents commonly used in the art, such as, for example, water or other solvents, solubilizing agents and emulsifiers, such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor and sesame oils), glycerol, tetrahydrofuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof.

[0213] Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, coloring, perfuming and preservative agents.

[0214] Suspensions, in addition to the active compounds, may contain suspending agents as, for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth, and mixtures thereof.

[0215] Formulations for rectal or vaginal administration may be presented as a suppository, which may be prepared by mixing one or more compounds of the invention with one or more suitable nonirritating excipients or carriers comprising, for example, cocoa butter, polyethylene glycol, a suppository wax or a salicylate, and which is solid at room temperature, but liquid at body temperature and, therefore, will melt in the rectum or vaginal cavity and release the active compound.

[0216] Formulations or dosage forms for the topical or transdermal administration of an oligomer as provided herein include powders, sprays, ointments, pastes, creams, lotions, gels, solutions, patches and inhalants. The active oligomers may be mixed under sterile conditions with a pharmaceutically-acceptable carrier, and with any preservatives, buffers, or propellants which may be required. The ointments, pastes, creams and gels may contain, in addition to an active compound of this invention, excipients, such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc and zinc oxide, or mixtures thereof.

[0217] Powders and sprays can contain, in addition to an oligomer of the present invention, excipients such as lactose,

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talc, silicic acid, aluminum hydroxide, calcium silicates and polyamide powder, or mixtures of these substances. Sprays can additionally contain customary propellants, such as chlorofluorohydrocarbons and volatile unsubstituted hydrocarbons, such as butane and propane.

[0218] Transdermal patches have the added advantage of providing controlled delivery of an oligomer of the present invention to the body. Such dosage forms can be made by dissolving or dispersing the oligomer in the proper medium. Absorption enhancers can also be used to increase the flux of the agent across the skin. The rate of such flux can be controlled by either providing a rate controlling membrane or dispersing the agent in a polymer matrix or gel, among other methods known in the art.

[0219] Pharmaceutical compositions suitable for parenteral administration may comprise one or more oligomers of the invention in combination with one or more pharmaceutically-acceptable sterile isotonic aqueous or nonaqueous solutions, dispersions, suspensions or emulsions, or sterile powders which may be reconstituted into sterile injectable solutions or dispersions just prior to use, which may contain sugars, alcohols, antioxidants, buffers, bacteriostats, solutes which render the formulation isotonic with the blood of the intended recipient or suspending or thickening agents. Examples of suitable aqueous and nonaqueous carriers which may be employed in the pharmaceutical compositions of the invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0220] These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of the action of microorganisms upon the subject oligomers may be ensured by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

[0221] In some cases, in order to prolong the effect of a drug, it is desirable to slow the absorption of the drug from subcutaneous or intramuscular injection. This may be accomplished by the use of a liquid suspension of crystalline or amorphous material having poor water solubility, among other methods known in the art. The rate of absorption of the drug then depends upon its rate of dissolution which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally-administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle.

[0222] Injectable depot forms may be made by forming microencapsule matrices of the subject oligomers in biodegradable polymers such as polylactide-polyglycolide. Depending on the ratio of oligomer to polymer, and the nature of the particular polymer employed, the rate of oligomer release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides).

Depot injectable formulations may also be prepared by entrapping the drug in liposomes or microemulsions that are compatible with body tissues.

[0223] When the oligomers of the present invention are administered as pharmaceuticals, to humans and animals, they can be given per se or as a pharmaceutical composition containing, for example, 0.1 to 99% (more preferably, 10 to 30%) of active ingredient in combination with a pharmaceutically acceptable carrier.

[0224] As noted above, the formulations or preparations of the present invention may be given orally, parenterally, topically, or rectally. They are typically given in forms suitable for each administration route. For example, they are administered in tablets or capsule form, by injection, inhalation, eye lotion, ointment, suppository, etc. administration by injection, infusion or inhalation; topical by lotion or ointment; and rectal by suppositories.

[0225] The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal and intrasternal injection and infusion.

[0226] The phrases "systemic administration," "administered systemically," "peripheral administration" and "administered peripherally" as used herein mean the administration of a compound, drug or other material other than directly into the central nervous system, such that it enters the patient's system and, thus, is subject to metabolism and other like processes, for example, subcutaneous administration.

[0227] Regardless of the route of administration selected, the oligomers of the present invention, which may be used in a suitable hydrated form, and/or the pharmaceutical compositions of the present invention, may be formulated into pharmaceutically-acceptable dosage forms by conventional methods known to those of skill in the art. Actual dosage levels of the active ingredients in the pharmaceutical compositions of this invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being unacceptably toxic to the patient.

[0228] The selected dosage level will depend upon a variety of factors including the activity of the particular oligomer of the present invention employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion or metabolism of the particular oligomer being employed, the rate and extent of absorption, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular oligomer employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0229] A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the effective amount of the pharmaceutical composition required. For example, the physician or veterinarian could start doses of the compounds of the invention employed in the pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved. In general, a

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suitable daily dose of a compound of the invention will be that amount of the compound which is the lowest dose effective to produce a therapeutic effect. Such an effective dose will generally depend upon the factors described above. Generally, oral, intravenous, intracerebroventricular and subcutaneous doses of the compounds of this invention for a patient, when used for the indicated effects, will range from about 0.0001 to about 100 mg per kilogram of body weight per day.

[0230] If desired, the effective daily dose of the active compound may be administered as two, three, four, five, six or more sub-doses administered separately at appropriate intervals throughout the day, optionally, in unit dosage forms. In certain situations, dosing is one administration per day. In certain embodiments, dosing is one or more administration per every 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 days, or every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 weeks, or every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 months, as needed, to maintain the desired expression of a functional dystrophin protein.

[0231] Nucleic acid molecules can be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres, as described herein and known in the art. In certain embodiments, microemulsification technology may be utilized to improve bioavailability of lipophilic (water insoluble) pharmaceutical agents. Examples include Trimetrine (Dordunoo, S. K., et al., *Drug Development and Industrial Pharmacy*, 17(12), 1685-1713, 1991 and REV 5901 (Sheen, P. C., et al., *J Pharm Sci* 80(7), 712-714, 1991). Among other benefits, microemulsification provides enhanced bioavailability by preferentially directing absorption to the lymphatic system instead of the circulatory system, which thereby bypasses the liver, and prevents destruction of the compounds in the hepatobiliary circulation.

[0232] In one aspect of invention, the formulations contain micelles formed from an oligomer as provided herein and at least one amphiphilic carrier, in which the micelles have an average diameter of less than about 100 nm. More preferred embodiments provide micelles having an average diameter less than about 50 nm, and even more preferred embodiments provide micelles having an average diameter less than about 30 nm, or even less than about 20 nm.

[0233] While all suitable amphiphilic carriers are contemplated, the presently preferred carriers are generally those that have Generally-Recognized-as-Safe (GRAS) status, and that can both solubilize the compound of the present invention and microemulsify it at a later stage when the solution comes into a contact with a complex water phase (such as one found in human gastro-intestinal tract). Usually, amphiphilic ingredients that satisfy these requirements have HLB (hydrophilic to lipophilic balance) values of 2-20, and their structures contain straight chain aliphatic radicals in the range of C-6 to C-20. Examples are polyethylene-glycolized fatty glycerides and polyethylene glycols.

[0234] Examples of amphiphilic carriers include saturated and monounsaturated polyethyleneglycolized fatty acid glycerides, such as those obtained from fully or partially hydrogenated various vegetable oils. Such oils may advantageously consist of tri-, di-, and mono-fatty acid glycerides and di- and mono-polyethyleneglycol esters of the corresponding fatty acids, with a particularly preferred fatty acid composition including capric acid 4-10, capric acid 3-9, lauric acid 40-50, myristic acid 14-24, palmitic acid 4-14 and stearic acid

5-15%. Another useful class of amphiphilic carriers includes partially esterified sorbitan and/or sorbitol, with saturated or mono-unsaturated fatty acids (SPAN-series) or corresponding ethoxylated analogs (TWEEN-series).

[0235] Commercially available amphiphilic carriers may be particularly useful, including Gelucire-series, Labrafil, Labrasol, or Lauroglycol (all manufactured and distributed by Gattefossé Corporation, Saint Priest, France), PEG-monooleate, PEG-di-oleate, PEG-mono-laurate and di-laurate, Lecithin, Polysorbate 80, etc (produced and distributed by a number of companies in USA and worldwide).

[0236] In certain embodiments, the delivery may occur by use of liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for the introduction of the compositions of the present invention into suitable host cells. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, a nanoparticle or the like. The formulation and use of such delivery vehicles can be carried out using known and conventional techniques.

[0237] Hydrophilic polymers suitable for use in the present invention are those which are readily water-soluble, can be covalently attached to a vesicle-forming lipid, and which are tolerated *in vivo* without toxic effects (i.e., are biocompatible). Suitable polymers include polyethylene glycol (PEG), polylactic (also termed polylactide), polyglycolic acid (also termed polyglycolide), a polylactic-polyglycolic acid copolymer, and polyvinyl alcohol. In certain embodiments, polymers have a molecular weight of from about 100 or 120 daltons up to about 5,000 or 10,000 daltons, or from about 300 daltons to about 5,000 daltons. In other embodiments, the polymer is polyethyleneglycol having a molecular weight of from about 100 to about 5,000 daltons, or having a molecular weight of from about 300 to about 5,000 daltons. In certain embodiments, the polymer is polyethyleneglycol of 750 daltons (PEG(750)). Polymers may also be defined by the number of monomers therein; a preferred embodiment of the present invention utilizes polymers of at least about three monomers, such PEG polymers consisting of three monomers (approximately 150 daltons).

[0238] Other hydrophilic polymers which may be suitable for use in the present invention include polyvinylpyrrolidone, polymethoxazoline, polyethyloxazoline, polyhydroxypropyl methacrylamide, polymethacrylamide, polydimethylacrylamide, and derivatized celluloses such as hydroxymethylcellulose or hydroxyethylcellulose.

[0239] In certain embodiments, a formulation of the present invention comprises a biocompatible polymer selected from the group consisting of polyamides, polycarbonates, polyalkylenes, polymers of acrylic and methacrylic esters, polyvinyl polymers, polyglycolides, polysiloxanes, polyurethanes and co-polymers thereof, celluloses, polypropylene, polyethylenes, polystyrene, polymers of lactic acid and glycolic acid, polyanhydrides, poly(ortho)esters, poly(butic acid), poly(valeric acid), poly(lactide-co-caprolactone), polysaccharides, proteins, polyhyaluronic acids, polycyanoacrylates, and blends, mixtures, or copolymers thereof.

[0240] Cyclodextrins are cyclic oligosaccharides, consisting of 6, 7 or 8 glucose units, designated by the Greek letter α , β , or γ , respectively. The glucose units are linked by α -1,4-glucosidic bonds. As a consequence of the chair conformation of the sugar units, all secondary hydroxyl groups (at C-2, C-3) are located on one side of the ring, while all the primary

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hydroxyl groups at C-6 are situated on the other side. As a result, the external faces are hydrophilic, making the cyclodextrins water-soluble. In contrast, the cavities of the cyclodextrins are hydrophobic, since they are lined by the hydrogen of atoms C-3 and C-5, and by ether-like oxygens. These matrices allow complexation with a variety of relatively hydrophobic compounds, including, for instance, steroid compounds such as 17 α -estradiol (see, e.g., van Uden et al. Plant Cell Tiss. Org. Cult. 38:1-3-113 (1994)). The complexation takes place by Van der Waals interactions and by hydrogen bond formation. For a general review of the chemistry of cyclodextrins, see, Wenz, Agnew. Chem. Int. Ed. Engl., 33:803-822 (1994).

[0241] The physico-chemical properties of the cyclodextrin derivatives depend strongly on the kind and the degree of substitution. For example, their solubility in water ranges from insoluble (e.g., triacetyl-beta-cyclodextrin) to 147% soluble (w/v) (G-2-beta-cyclodextrin). In addition, they are soluble in many organic solvents. The properties of the cyclodextrins enable the control over solubility of various formulation components by increasing or decreasing their solubility.

[0242] Numerous cyclodextrins and methods for their preparation have been described. For example, Parmeter (I), et al. (U.S. Pat. No. 3,453,259) and Gramera, et al. (U.S. Pat. No. 3,459,731) described electroneutral cyclodextrins. Other derivatives include cyclodextrins with cationic properties [Parmeter (II), U.S. Pat. No. 3,453,257], insoluble crosslinked cyclodextrins (Solms, U.S. Pat. No. 3,420,788), and cyclodextrins with anionic properties [Parmeter (III), U.S. Pat. No. 3,426,011]. Among the cyclodextrin derivatives with anionic properties, carboxylic acids, phosphorous acids, phosphoinous acids, phosphonic acids, phosphoric acids, thiophosphonic acids, thiosulphinic acids, and sulfonic acids have been appended to the parent cyclodextrin [see, Parmeter (III), *supra*]. Furthermore, sulfoalkyl ether cyclodextrin derivatives have been described by Stella, et al. (U.S. Pat. No. 5,134,127).

[0243] Liposomes consist of at least one lipid bilayer membrane enclosing an aqueous internal compartment. Liposomes may be characterized by membrane type and by size. Small unilamellar vesicles (SUVs) have a single membrane and typically range between 0.02 and 0.05 μm in diameter; large unilamellar vesicles (LUVS) are typically larger than 0.05 μm . Oligolamellar large vesicles and multilamellar vesicles have multiple, usually concentric, membrane layers and are typically larger than 0.1 μm . Liposomes with several nonconcentric membranes, i.e., several smaller vesicles contained within a larger vesicle, are termed multivesicular vesicles.

[0244] One aspect of the present invention relates to formulations comprising liposomes containing an oligomer of the present invention, where the liposome membrane is formulated to provide a liposome with increased carrying capacity. Alternatively or in addition, the compound of the present invention may be contained within, or adsorbed onto, the liposome bilayer of the liposome. An oligomer of the present invention may be aggregated with a lipid surfactant and carried within the liposome's internal space; in these cases, the liposome membrane is formulated to resist the disruptive effects of the active agent-surfactant aggregate.

[0245] According to one embodiment of the present invention, the lipid bilayer of a liposome contains lipids derivatized with polyethylene glycol (PEG), such that the PEG chains

extend from the inner surface of the lipid bilayer into the interior space encapsulated by the liposome, and extend from the exterior of the lipid bilayer into the surrounding environment.

[0246] Active agents contained within liposomes of the present invention are in solubilized form. Aggregates of surfactant and active agent (such as emulsions or micelles containing the active agent of interest) may be entrapped within the interior space of liposomes according to the present invention. A surfactant acts to disperse and solubilize the active agent, and may be selected from any suitable aliphatic, cycloaliphatic or aromatic surfactant, including but not limited to biocompatible lysophosphatidylcholines (LPGs) of varying chain lengths (for example, from about C14 to about C20). Polymer-derivatized lipids such as PEG-lipids may also be utilized for micelle formation as they will act to inhibit micelle/membrane fusion, and as the addition of a polymer to surfactant molecules decreases the CMC of the surfactant and aids in micelle formation. Preferred are surfactants with CMOs in the micromolar range; higher CMC surfactants may be utilized to prepare micelles entrapped within liposomes of the present invention.

[0247] Liposomes according to the present invention may be prepared by any of a variety of techniques that are known in the art. See, e.g., U.S. Pat. No. 4,235,871; Published PCT applications WO 96/14057; New RRC, *Liposomes: A practical approach*, IRL Press, Oxford (1990), pages 33-104; Lasic DD, *Liposomes from physics to applications*, Elsevier Science Publishers BV, Amsterdam, 1993. For example, liposomes of the present invention may be prepared by diffusing a lipid derivatized with a hydrophilic polymer into preformed liposomes, such as by exposing preformed liposomes to micelles composed of lipid-grafted polymers, at lipid concentrations corresponding to the final mole percent of derivatized lipid which is desired in the liposome. Liposomes containing a hydrophilic polymer can also be formed by homogenization, lipid-field hydration, or extrusion techniques, as are known in the art.

[0248] In another exemplary formulation procedure, the active agent is first dispersed by sonication in a lysophosphatidylcholine or other low CMC surfactant (including polymer grafted lipids) that readily solubilizes hydrophobic molecules. The resulting micellar suspension of active agent is then used to rehydrate a dried lipid sample that contains a suitable mole percent of polymer-grafted lipid, or cholesterol. The lipid and active agent suspension is then formed into liposomes using extrusion techniques as are known in the art, and the resulting liposomes separated from the unencapsulated solution by standard column separation.

[0249] In one aspect of the present invention, the liposomes are prepared to have substantially homogeneous sizes in a selected size range. One effective sizing method involves extruding an aqueous suspension of the liposomes through a series of polycarbonate membranes having a selected uniform pore size; the pore size of the membrane will correspond roughly with the largest sizes of liposomes produced by extrusion through that membrane. See e.g., U.S. Pat. No. 4,737,323 (Apr. 12, 1988). In certain embodiments, reagents such as DharmaFECT® and Lipofectamine® may be utilized to introduce polynucleotides or proteins into cells.

[0250] The release characteristics of a formulation of the present invention depend on the encapsulating material, the concentration of encapsulated drug, and the presence of release modifiers. For example, release can be manipulated to

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be pH dependent, for example, using a pH sensitive coating that releases only at a low pH, as in the stomach, or a higher pH, as in the intestine. An enteric coating can be used to prevent release from occurring until after passage through the stomach. Multiple coatings or mixtures of cyanamide encapsulated in different materials can be used to obtain an initial release in the stomach, followed by later release in the intestine. Release can also be manipulated by inclusion of salts or pore forming agents, which can increase water uptake or release of drug by diffusion from the capsule. Excipients which modify the solubility of the drug can also be used to control the release rate. Agents which enhance degradation of the matrix or release from the matrix can also be incorporated. They can be added to the drug, added as a separate phase (i.e., as particulates), or can be co-dissolved in the polymer phase depending on the compound. In most cases the amount should be between 0.1 and thirty percent (w/w polymer). Types of degradation enhancers include inorganic salts such as ammonium sulfate and ammonium chloride, organic acids such as citric acid, benzoic acid, and ascorbic acid, inorganic bases such as sodium carbonate, potassium carbonate, calcium carbonate, zinc carbonate, and zinc hydroxide, and organic bases such as protamine sulfate, spermine, choline, ethanolamine, diethanolamine, and triethanolamine and surfactants such as Tween® and Pluronic®. Pore forming agents which add microstructure to the matrices (i.e., water soluble compounds such as inorganic salts and sugars) are added as particulates. The range is typically between one and thirty percent (w/w polymer).

[0251] Uptake can also be manipulated by altering residence time of the particles in the gut. This can be achieved, for example, by coating the particle with, or selecting as the encapsulating material, a mucosal adhesive polymer. Examples include most polymers with free carboxyl groups, such as chitosan, celluloses, and especially polyacrylates (as used herein, polyacrylates refers to polymers including acrylate groups and modified acrylate groups such as cyanoacrylates and methacrylates).

[0252] An oligomer may be formulated to be contained within, or, adapted to release by a surgical or medical device or implant. In certain aspects, an implant may be coated or otherwise treated with an oligomer. For example, hydrogels, or other polymers, such as biocompatible and/or biodegradable polymers, may be used to coat an implant with the compositions of the present invention (i.e., the composition may be adapted for use with a medical device by using a hydrogel or other polymer). Polymers and copolymers for coating medical devices with an agent are well-known in the art. Examples of implants include, but are not limited to, stents, drug-eluting stents, sutures, prosthesis, vascular catheters, dialysis catheters, vascular grafts, prosthetic heart valves, cardiac pacemakers, implantable cardioverter defibrillators, IV needles, devices for bone setting and formation, such as pins, screws, plates, and other devices, and artificial tissue matrices for wound healing.

[0253] In addition to the methods provided herein, the oligomers for use according to the invention may be formulated for administration in any convenient way for use in human or veterinary medicine, by analogy with other pharmaceuticals. The antisense oligomers and their corresponding formulations may be administered alone or in combination with other

therapeutic strategies in the treatment of muscular dystrophy, such as myoblast transplantation, stem cell therapies, administration of aminoglycoside antibiotics, proteasome inhibitors, and up-regulation therapies (e.g., upregulation of utrophin, an autosomal parologue of dystrophin).

[0254] All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

[0255] Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims. The following examples are provided by way of illustration only and not by way of limitation. Those of skill in the art will readily recognize a variety of noncritical parameters that could be changed or modified to yield essentially similar results.

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EXAMPLES

Materials and Methods

- [0277] Cells and Tissue Culture Treatment Conditions
- [0278] Human Rhabdomyosarcoma cells (ATCC, CCL-136; RD cells) preserved in a 5% DMSO solution (Sigma) at a low passage number were thawed in a 37°C water bath until the ice sliver was no longer visible. Cells were seeded into tissue culture-treated T75 flasks (Nunc) at 1.5×10⁶ cells/flask in 24 mL of warmed DMEM with L-Glutamine (HyClone), 10% fetal bovine serum, and 1% Penicillin-Streptomycin antibiotic solution (CelGro); after 24 hours, media was aspirated, cells were washed once in warmed PBS, and fresh media was added. Cells were grown to 80% confluence in a 37°C incubator at 5.0% CO₂.

[0279] Media was aspirated from T75 flasks; cells were washed once in warmed PBS and aspirated. 3 mL of Trypsin/EDTA, warmed in a 37°C water bath, was added to each T75. Cells were incubated at 37°C 5-2 minutes until, with gentle agitation, they released from the flask. Cell suspension was transferred to a 15.0 mL conical tube; flasks were rinsed with 1.0 mL of Trypsin/EDTA solution to gather remaining cells. Cells were counted with a Vi-Cell XR cell counter (Beckman Coulter). Cells were seeded into tissue culture-treated 12-well plates (Falcon) at 2.0×10⁵ viable cells per well in 1.0 mL media. Cells were incubated overnight in a 37°C incubator at 5.0% CO₂.

[0280] Twelve-well seeded plates were examined for even cellular distribution and plate adherence. Lyophilized peptide conjugated phosphorodiamidate morpholino oligomers (PPMOs) were re-suspended at 2.0 mM in nuclease-free water (Ambion), and kept on ice during cell treatment; to verify molarity, PPMOs were measured using a Nanoprop 2000 spectrophotometer (Thermo Scientific). Immediately prior to PPMO treatment, media was aspirated, and cells were rinsed in warmed PBS. PPMOs were diluted in warmed media to the desired molarity; cells were treated in a total of 1.0 mL PPMO per well. PPMOs were tested in triplicate. For no-treatment controls, fresh, warmed media was added in 1.0 mL total volume. Cells were incubated for 48 hours in a 37°C incubator at 5.0% CO₂.

[0281] RNA Extraction

[0282] Media was aspirated, and cells were rinsed in warmed PBS. RNA was extracted with the QuickGene-Mini80 system, QuickGene RNA cultured cell HC kit S, and MagNAlyser with ceramic bead homogenization using the manufacturers' recommended protocols. Briefly, cells were lysed in treatment plates with 350 uL LRP (10 uL β-Mercaptoethanol added per 100 uL LRP) lysis buffer; homogenate was gently triturated to ensure full lysis, and transferred to MagNAlyser tubes. Tubes were spun at 2800 rpm for 30 seconds in the MagNAlyser to ensure full homogenization, and iced briefly. 50 uL SRP solubilization buffer was added and homogenate was vortexed for 15 seconds. 170 uL >99% ethanol was added to each tube, and homogenate was vortexed for 60 seconds. Homogenate was flash-spun and transferred to Mini80 RNA cartridges, samples were pressurized and flow-through was discarded. Cartridges were washed in 750 uL WRP wash buffer and pressurized. 40 uL of DNase solution (1.25 uL Qiagen DNasel, 35 uL RDD Buffer, 3.75 uL nuclease-free water) was added directly to the cartridge membrane; cartridges were incubated four minutes at room temperature. Cartridges were washed twice with 750 uL WRP, pressurizing after each wash. Cartridges were placed over nuclease-free tubes. 50 uL CRP elution buffer was added to each membrane; membranes were incubated for five minutes at room-temperature. Cartridges were pressurized and eluate was collected. RNA was stored at -80°C pending quantification. RNA was quantified using the Nanoprop™ 2000 spectrophotometer.

[0283] Nested RT-PCR

[0284] Primer-specific, exon-specific, optimized nested RT-PCR amplification was performed using the primer pair sets for each dystrophin exon as shown below in Table 1.

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TABLE 1

Primer pair sets used to PCR amplify human dystrophin mRNA to detect exon-skipping.						
Name	F/R	I/O	Sequence (5'-3')	Exon Purpose	SEQ ID NO:	
PS170	F	O	CCAGAGCTTACCTGAGAACAAAG	48 Detection	640	
PS172	F	I	CCAGGCCACTCAGCCAGTGAGG	49 of Exon 50	641	
PS174	R	I	CGATCCGTAAATGATTGTTCTAGCC	52 and 51	642	
PS176	R	O	CATTTCACTCAACTGTTGCCTCCG	53 Skipping in Human Dystrophin	643	
PS186	F	O	CAATGCTCCTGACCTCTGTGC	42 Detection	644	
PS187	F	I	GCTCTACAAACAAAGCTCAGGTGCG	43 of Exon 44	645	
PS189	F	I	GCAATGTTATCTGCTTCCTCCAACC	46 and 45	646	
PS190	R	O	GCTCTTTCCAGGTTCAAGTGG	46 Skipping in Human Dystrophin	647	
PS192	F	O	CTTGGACAGAACTTACCGACTGCG	51 Detection	648	
PS193	F	I	GCAGGATTGGAACAGAGGCG	52 of Exon 53	649	
PS195	R	I	CATCTACATTGTCTGCCACTGCG	54 Skipping in	650	
PS197	R	O	GTTTCTTCCAAAGCAGCCTCTCG	55 Human Dystrophin	651	

[0285] The indicated primer pairs are shown as either forward or reverse (F/R) and either outer or inner primer pairs (I/O) corresponding to primary or secondary amplifications, respectively. The location of the primer target is indicated in the Exon column and the Purpose indicates the exon-skipping events can be detected. For example, PS170 and PS176 primers amplify a region from exon 48 to 53 in the primary amplification. Primers PS172 and PS174 then amplify a region from exon 49 to 52 in the secondary amplification. This nested PCR reaction will detect exon skipping of both exons 50 and/or exon 51. The specific nested RT-PCR reaction conditions are provided below.

[0286] RNA extracted from treated cells (described above) was diluted to 20 ng/ μ l for all samples.

TABLE 2

Reaction setup for RT-PCR and primary amplification (50 μ l reaction):	
2x Reaction mix	25 μ l
PS XXX Forward Primer (30 μ M) (see Table 1)	0.5 μ l
PS XXX Reverse Primer (30 μ M) (see Table 1)	0.5 μ l
Superscript III Platinum Taq mix	2 μ l
Template RNA (20 ng/ μ l)	10 μ l
Nuclease-Free Water (50 μ l total volume)	12 μ l

TABLE 3

RT-PCR and primary amplification program:		
	Temperature	Time
Reverse Transcription	55° C.	30 minutes
RT Inactivation	94° C.	2 minutes
Denaturing	94° C.	1 minute
Annealing	59° C.	1 minute
		8 Cycles

TABLE 3-continued

RT-PCR and primary amplification program:		
	Temperature	Time
Extension	68° C.	1 minute
	4° C.	∞

TABLE 4

Reaction setup for nested secondary amplification (50 μ l reaction):	
10x PCR Buffer	5 μ l
dNTP solution (10 mM)	0.5 μ l
50 mM MgCl ₂	1.5 μ l
PS XXX Forward Primer (30 μ M) (see Table 1)	0.33 μ l
PS XXX Reverse Primer (30 μ M) (see Table 1)	0.33 μ l
Platinum Taq DNA polymerase	0.2 μ l
0.1 mM Cy5-dCTP	1 μ l
RT-PCR product (from Step 1)	1 μ l
Nuclease-Free Water (50 μ l total volume)	40.15 μ l

TABLE 5

Nested secondary amplification program:		
	Temperature	Time
Primary Denature	94° C.	3 minutes
Denaturing	94° C.	45 seconds
Annealing	59° C.	30 seconds
Extension	68° C.	1 minute
	4° C.	∞
		Cycles

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[0287] Gel Electrophoresis Analysis

[0288] Ten microliters of 5× Ficoll loading dye was added to each 50 microliter nested RT-PCR reaction. Fifteen microliters of PCR/dye mixture was run on a 10% TBE gel at 300 volts for 30 minutes. After electrophoresis, the gel was washed in diH₂O for at least one hour, changing the water every 30 minutes. The gel was then scanned on a Typhoon Trio Variable Mode Imager (GE Healthcare). For exon 44 skipping, the nested RT-PCR product from full-length dystrophin transcript is 571 bp, and 423 bp from Exon 44-skipped mRNA (exon 44 is 148 bp). For exon 45, the nested RT-PCR product from full-length dystrophin transcript is 571 bp, and 395 bp from Exon 45-skipped mRNA (exon 45 is 176 bp). For exon 53, the PCR product from full-length dystrophin transcript is 365 bp, and 153 bp from exon 53-skipped mRNA (exon 53 is 212 bp).

[0289] The gel images were subjected to quantitative analysis by measuring the band intensities of the full-length PCR product compared to the exon-skipped product. In some cases, the percent skipping at a fixed PPMO concentration (e.g., 3 micromolar) was used to determine the relative activity of a series of PPMO to induce exon skipping of a given exon. In other situations, a PPMO dose-range was used to treat cells (e.g., 0.1, 0.3, 1.0, 3.0 and 10 micromolar) and an EC₅₀ was calculated based on the percent skipping induced at each concentration.

Example 1

Exon 51 Scan

[0290] A series of overlapping antisense PPMOs that target human dystrophin exon 51 were designed, synthesized and used to treat either human rhabdomyosarcoma cells (RD cells) or primary human skeletal muscle cells. This strategy is termed an “exon scan” and was used similarly for several other dystrophin exons as described below. All the PPMOs were synthesized as peptide-conjugated PMO (PPMO) using the CP06062 peptide (SEQ ID NO: 578) and a 3' terminal PMO linkage. For exon 51, a series of 26 PPMOs, each 26 bases in length, were made (SEQ ID NOS: 309-311, 314, 316, 317, 319, 321, 323, 324, 326, 327, 329-331, 333, 335, 336, 338-345) as shown in FIG. 2A. The PPMOs were evaluated for exon skipping efficacy by treating RD cells at various concentrations as described above in the Materials and Methods. Three PPMOs (SEQ ID NOS: 324, 326 and 327) were identified as effective in inducing exon-skipping and selected for additional evaluation. Dose-ranging experiments in RD cells and primary human skeletal muscle cells were used to confirm the relative efficacy of these three PPMO sequences. SEQ ID NO: 327 was shown to be most effective at inducing exon 51 skipping as shown in FIGS. 2B and 2C.

[0291] A comparison of the relative effectiveness of SEQ ID NO: 327 to other exon 51-targeted antisense sequences was performed in RD cells and primary human skeletal muscle cells, as described above. All the evaluated sequences were made as peptide-conjugated PMOs using the CP06062 peptide (SEQ ID NO: 578). This allowed direct comparison of the relative effectiveness of the antisense sequences without regard to antisense chemistry or cell delivery. The relative location of the certain exon 51-targeted oligos compared to SEQ ID NO: 327 is shown in FIG. 2D. As shown in FIG. 2C, there is a ranked hierarchy of exon-skipping effectiveness,

with SEQ ID NO: 327 being the most effective by at least a factor of several-fold compared to other sequences.

Example 2

Exon 50 Scan

[0292] A series of overlapping antisense PPMOs that target human dystrophin exon 50 were designed and synthesized. For exon 50, a series of 17 PPMOs, each 25 bases in length, were made (SEQ ID NOS: 267, 269, 271, 273, 275, 277, 279, 280, 282 and 284-291) as shown in FIG. 3A. The PPMOs were evaluated for exon skipping efficacy by treating RD cells at various concentrations as described above in the Materials and Methods. Four PPMOs (SEQ ID NOS: 277, 287, 290 and 291) were identified as effective in inducing exon-skipping and selected for additional evaluation. Dose-ranging experiments in RD cells were used to confirm the relative efficacy of these four PMO sequences. SEQ ID NOS: 584 (AVI-5656) and 287 (AVI-5038) were shown to be most effective at inducing exon 50 skipping as shown in FIG. 3B. The EC₅₀ values were derived from the dose-ranging experiments and represent the calculated concentration where 50% of the PCR product is from the mRNA lacking exon 50 relative to the PCR product produced from the mRNA containing exon 50. Compared to other sequences (see, e.g., SEQ ID NOS: 584 and 585 correspond to SEQ ID NOS: 173 and 175 in WO2006/000057, respectively) AVI-5038 (SEQ ID NO: 287) is equivalent or better at inducing exon-skipping activity in the RD cell assay as shown in FIG. 3B.

Example 3

Exon 53 Scan

[0293] A series of overlapping antisense PPMOs that target human dystrophin exon 53 were designed and synthesized. For exon 53, a series of 24 PPMOs, each 25 bases in length, were made (SEQ ID NOS: 416, 418, 420, 422, 424, 426, 428, 429, 431, 433, 434, 436, 438-440 and 443-451) as shown in FIG. 4A. The PPMOs were evaluated for exon skipping efficacy by treating RD cells and primary human skeletal muscle cells at various concentrations as described above in the Materials and Methods. Three PPMOs (SEQ ID NOS: 428, 429 and 431) were identified as effective in inducing exon-skipping and selected for additional evaluation. Dose-ranging experiments in RD cells were used to confirm the relative efficacy of these three PMO sequences. SEQ ID NO: 429 was shown to be most effective at inducing exon 53 skipping as shown in FIGS. 4B-F. However, when compared to other exon 53 antisense sequences, SEQ ID NO: 429 proved identical to H53A(+23+47) which is listed as SEQ ID NO: 195 in WO2006/000057 and SEQ ID NO: 609 in the present application. Other sequences were compared to SEQ ID NO: 429 including H53A(+39+69) and H53A(-12+10) (listed as SEQ ID NOS: 193 and 199 in WO2006/000057, respectively) and h53AON1 (listed as SEQ ID NO: 39 in U.S. application Ser. No. 11/233,507) and listed as SEQ ID NOS: 608, 611 and 610, respectively, in the present application. All the evaluated sequences were made as peptide-conjugated PMOs using the CP06062 peptide (SEQ ID NO: 578). This allowed direct comparison of the relative effectiveness of the antisense sequences without regard to antisense chemistry or cell deliv-

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ery. As shown in FIGS. 4I and 4G-H, SEQ ID NO: 429 was shown to be superior to each of these four sequences.

Example 4
Exon 44 Scan

[0294] A series of overlapping antisense PPMOs that target human dystrophin exon 44 were designed and synthesized. For exon 44, a series of PPMOs, each 25 bases in length, were made (SEQ ID NOS: 1-20) as shown in FIG. 5A. The PPMOs were evaluated for exon skipping efficacy by treating RD cells at various concentrations as described above in the Materials and Methods. Five PPMOs (SEQ ID NOS: 4, 8, 11, 12 and 13) were identified as effective in inducing exon-skipping and selected for additional evaluation. Dose-ranging experiments in RD cells were used to confirm the relative efficacy of these five PPMO sequences as shown in FIGS. 5C to 5H. SEQ ID NOS: 8, 11 and 12 were shown to be most effective at inducing exon 44 skipping as shown in FIG. 5H with SEQ ID NO: 12 proving the most efficacious.

[0295] Comparison of SEQ ID NO: 12 to other exon 44 antisense sequences was done in both RD cells and human primary skeletal muscle cells. All the evaluated sequences were made as peptide-conjugated PMOs using the CP06062 peptide (SEQ ID NO: 578). This allowed direct comparison of the relative effectiveness of the antisense sequences without regard to antisense chemistry or cell delivery.

[0296] The alignment of the sequences (SEQ ID NOS: 600, 601, 602 and 603) with SEQ ID NOS: 4, 8, 11 and 12 is shown in FIG. 5B. SEQ ID NOS: 601 and 603 are listed as SEQ ID NOS: 165 and 167 in WO2006/000057. SEQ ID NO: 602 is listed in WO2004/083446 and as SEQ ID NO: 21 in U.S. application Ser. No. 11/233,507. SEQ ID NO: 600 was published in 2007 (Wilton, Fall et al. 2007). The comparison in RD cells showed that both SEQ ID NOS: 602 and 603 were superior to SEQ ID NO: 12 (FIG. 5I). However, as shown in FIG. 5J, in human primary skeletal muscle cells SEQ ID NO: 12 was superior (8.86% exon skipping) to SEQ ID NO: 602 (6.42%). Similar experiments are performed with SEQ ID NO: 603.

Example 5
Exon 45 Scan

[0297] A series of overlapping antisense PPMOs that target human dystrophin exon 45 were designed and synthesized.

For exon 45, a series of 22 PPMOs, each 25 bases in length, were made (SEQ ID NOS: 21, 23, 25, 27, 29, 31, 32, 34, 35, 37, 39, 41, 43 and 45-53) as shown in FIG. 6A. The PPMOs were evaluated for exon skipping efficacy by treating RD cells and human primary skeletal muscle cells at various concentrations as described above in the Materials and Methods. Five PPMOs (SEQ ID NOS: 27, 29, 34, and 39) were identified as effective in inducing exon-skipping and selected for additional evaluation. Dose-ranging experiments in RD cells were used to confirm the relative efficacy of these four PMO sequences as shown in FIGS. 6C-G and summarized in FIG. 6H. SEQ ID NO: 49 was used as a negative control in these experiments. SEQ ID NOS: 29 and 34 were shown to be most effective at inducing exon 45 skipping as shown in FIG. 6H.

[0298] Comparison of SEQ ID NO: 34 to other exon 45 antisense sequences was done in both RD cells and human primary skeletal muscle cells. All the evaluated sequences were made as peptide-conjugated PMOs using the CP06062 peptide (SEQ ID NO: 578). This allowed direct comparison of the relative effectiveness of the antisense sequences without regard to antisense chemistry or cell delivery. The alignment of the sequences (SEQ ID NOS: 604, 605, 606 and 607) with SEQ ID NOS: 27, 29, 34 and 39 is shown in FIG. 6B. SEQ ID NOS: 604 and 607 are listed as SEQ ID NOS: 211 and 207 in WO2006/000057, respectively. SEQ ID NOS: 605 and 606 are listed in U.S. application Ser. No. 11/233,507 as SEQ ID NOS: 23 and 1, respectively. The comparison in RD cells showed that SEQ ID NO: 34 was superior to all four sequences evaluated as shown in FIG. 6I. Testing of these compounds in different populations of human primary skeletal muscle cells is performed as described above.

SEQUENCE ID LISTING

[0299] Sequences are shown using the nucleotide base symbols common for DNA: A, G, C and T. Other antisense chemistries such as 2'-O-methyl use U in place of T. Any of the bases may be substituted with inosine (I) especially in stretches of three or more G residues.

Name	Sequences	SEQ ID NO.
<u>Oligomer Targeting Sequences (5' to 3'):</u>		
Hu . DMD . Exon44 . 25 . 001	CTGCAGGTAAAAGCATATGGATCAA	1
Hu . DMD . Exon44 . 25 . 002	ATCGCCTGCAGGTAAAAGCATATGG	2
Hu . DMD . Exon44 . 25 . 003	GTCAAATCGCCTGCAGGTAAAAGCA	3
Hu . DMD . Exon44 . 25 . 004	GATCTGTCAAATGCCCTGCAGGTAA	4
Hu . DMD . Exon44 . 25 . 005	CAACAGATCTGTCAAATGCCCTGCA	5
Hu . DMD . Exon44 . 25 . 006	TTTCTCAACAGATCTGTCAAATCGC	6
Hu . DMD . Exon44 . 25 . 007	CCATTCTCAACAGATCTGTCAAAT	7
Hu . DMD . Exon44 . 25 . 008	ATAATGAAAACGCCGCCATTCTCA	8
Hu . DMD . Exon44 . 25 . 009	AAATATCTTATATCATAATGAAA	9

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon44.25.010	TGTTAGCCACTGATTAATATCTTT	10
Hu.DMD.Exon44.25.011	AAACTGTTCACTCTGTAGCCAC	11
Hu.DMD.Exon44.25.012	TTGTGTCTTCTGAGAACTGTTCA	12
Hu.DMD.Exon44.25.013	CCAATTCTCAGGAATTGTGTCTTT	13
Hu.DMD.Exon44.25.014	GTATTTAGCATGTTCCCAATTCTCA	14
Hu.DMD.Exon44.25.015	CTTAAGATACCATTGTATTAGCA	15
Hu.DMD.Exon44.25.016	CTTACCTTAAGATAACCATTGTATT	16
Hu.DMD.Exon44.25.017	AAAGACTTACCTTAAGATACCATT	17
Hu.DMD.Exon44.25.018	AAATCAAAGACTTACCTTAAGATAC	18
Hu.DMD.Exon44.25.019	AAAACAAATCAAAGACTTACCTTAA	19
Hu.DMD.Exon44.25.020	TCGAAAAAACAAATCAAAGACTTAC	20
Hu.DMD.Exon45.25.001	CTGTAAGATAACCAAAAGGCAAAAC	21
Hu.DMD.Exon45.25.002	CCTGTAAGATAACCAAAAGGCAAAA	22
Hu.DMD.Exon45.25.002.2	AGTTCCCTGTAAGATAACCAAAAGGC	23
Hu.DMD.Exon45.25.003	GAGTTCCCTGTAAGATAACCAAAAGG	24
Hu.DMD.Exon45.25.003.2	CCTGGAGTTCCCTGTAAGATAACCAA	25
Hu.DMD.Exon45.25.004	TCCTGGAGTTCCCTGTAAGATAACCAA	26
Hu.DMD.Exon45.25.004.2	GCCATCCTGGAGTTCCCTGTAAGATA	27
Hu.DMD.Exon45.25.005	TGCCATCCTGGAGTTCCCTGTAAGAT	28
Hu.DMD.Exon45.25.005.2	CCAATGCCATCCTGGAGTTCCCTGTA	29
Hu.DMD.Exon45.25.006	CCCAATGCCATCCTGGAGTTCCCTGT	30
Hu.DMD.Exon45.25.006.2	GCTGCCAATGCCATCCTGGAGTTTC	31
Hu.DMD.Exon45.25.007	CGCTGCCAATGCCATCCTGGAGTT	32
Hu.DMD.Exon45.25.008	AACAGTTGCCGCTGCCAATGCCA	33
Hu.DMD.Exon45.25.008.2	CTGACAACAGTTGCCGCTGCCAA	34
Hu.DMD.Exon45.25.009	GTTGCATTCAATGTTCTGACAACAG	35
Hu.DMD.Exon45.25.010	GCTGAATTATTCCTCCCCAGTTGCATTCA	36
Hu.DMD.Exon45.25.010.2	ATTATTCCTCCCCAGTTGCATTCA	37
Hu.DMD.Exon45.25.011	GGCATCTGTTTGAGGATTGCTGA	38
Hu.DMD.Exon45.25.011.2	TTTGAGGATTGCTGAATTATTCCTT	39
Hu.DMD.Exon45.25.012	AATTTTCCTGAGAATACTGGCAT	40
Hu.DMD.Exon45.25.012.2	ATACTGGCATCTGTTTGAGGATT	41
Hu.DMD.Exon45.25.013	ACCGCAGATTCAAGCTCCCAATT	42
Hu.DMD.Exon45.25.013.2	AATTTTCCTGAGAATACTGGCAT	43
Hu.DMD.Exon45.25.014	CTGTTGCAGACCTCCGCCACCGC	44
Hu.DMD.Exon45.25.014.2	AGATTCAGGCTTCCCAATTTCCT	45
Hu.DMD.Exon45.25.015	CTCTTTCTGCTGACAGCTGTT	46

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon45.25.015.2	ACCTCCTGCCACCGCAGATTCAAGGC	47
Hu.DMD.Exon45.25.016	CCTACCTTTTTCTGTCTGACAG	48
Hu.DMD.Exon45.25.016.2	GACAGCTGTTGCAGACCTCCTGCC	49
Hu.DMD.Exon45.25.017	GTCGCCCTACCTCTTTTCTGTCT	50
Hu.DMD.Exon45.25.018	GATCTGTCGCCCTACCTCTTTTC	51
Hu.DMD.Exon45.25.019	TATTAGATCTGTCGCCCTACCTCTT	52
Hu.DMD.Exon45.25.020	ATTCCTATTAGATCTGTCGCCCTAC	53
Hu.DMD.Exon45.20.001	AGATAACAAAAAGGCAAAAC	54
Hu.DMD.Exon45.20.002	AAGATAACAAAAAGGCAAAA	55
Hu.DMD.Exon45.20.003	CCTGTAAGATAACAAAAAGG	56
Hu.DMD.Exon45.20.004	GAGTCCTGTAAGATAACCAA	57
Hu.DMD.Exon45.20.005	TCCTGGAGTTCTGTAAAGAT	58
Hu.DMD.Exon45.20.006	TGCCATCCTGGAGTTCTGT	59
Hu.DMD.Exon45.20.007	CCCAATGCCATCCTGGAGTT	60
Hu.DMD.Exon45.20.008	CGCTGCCAATGCCATCCTG	61
Hu.DMD.Exon45.20.009	CTGACAACAGTTGCCGCTG	62
Hu.DMD.Exon45.20.010	GTTGCATTCAATGTTCTGAC	63
Hu.DMD.Exon45.20.011	ATTATTTCTCCCCAGTTGC	64
Hu.DMD.Exon45.20.012	TTTGAGGATTGCTGAATTAT	65
Hu.DMD.Exon45.20.013	ATACTGGCATCTGTTTTGA	66
Hu.DMD.Exon45.20.014	AATTTTCCTGTAGAATACT	67
Hu.DMD.Exon45.20.015	AGATTCAAGGCTTCCAATT	68
Hu.DMD.Exon45.20.016	ACCTCCTGCCACCGCAGATT	69
Hu.DMD.Exon45.20.017	GACAGCTGTTGCAGACCTC	70
Hu.DMD.Exon45.20.018	CTCTTTTCTGTCTGACAG	71
Hu.DMD.Exon45.20.019	CCTACCTCTTTTCTGTCT	72
Hu.DMD.Exon45.20.020	GTCGCCCTACCTCTTTTC	73
Hu.DMD.Exon45.20.021	GATCTGTCGCCCTACCTCTT	74
Hu.DMD.Exon45.20.022	TATTAGATCTGTCGCCCTAC	75
Hu.DMD.Exon45.20.023	ATTCCTATTAGATCTGTCGC	76
Hu.DMD.Exon46.25.001	GGGGGATTGAGAAAATAAAATTAC	77
Hu.DMD.Exon46.25.002	ATTTGAGAAAATAAAATTACCTTGA	78
Hu.DMD.Exon46.25.002.2	CTAGCCTGGAGAAAGAAGAATAAA	79
Hu.DMD.Exon46.25.003	AGAAAATAAAATTACCTTGACTTGC	80
Hu.DMD.Exon46.25.003.2	TTCTTCTAGCCTGGAGAAAAGAAGAA	81
Hu.DMD.Exon46.25.004	ATAAAATTACCTTGACTTGCTCAAG	82
Hu.DMD.Exon46.25.004.2	TTTTGTTCTTAGCCTGGAGAAAAG	83

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon46.25.005	ATTACCTTGACTTGCTCAAGCTTT	84
Hu.DMD.Exon46.25.005.2	TATTCTTTGTTCTTCTAGCCTGGA	85
Hu.DMD.Exon46.25.006	CTTGACTTGCTCAAGCTTTCTTT	86
Hu.DMD.Exon46.25.006.2	CAAGATATTCTTTGTTCTTAGC	87
Hu.DMD.Exon46.25.007	CTTTTAGTTGCTGCTTTCCAGG	88
Hu.DMD.Exon46.25.008	CCAGGTTCAAGTGGGATACTAGCAA	89
Hu.DMD.Exon46.25.008.2	ATCTCTTGAAATTCTGACAAGATA	90
Hu.DMD.Exon46.25.009	AGCAATGTTATCTGCTTCCTCCAAC	91
Hu.DMD.Exon46.25.009.2	AACAAATTCAATTAAATCTTTGA	92
Hu.DMD.Exon46.25.010	CCAACCATAAAACAAATTCAATTAA	93
Hu.DMD.Exon46.25.010.2	TTCCTCCAACCATAAAACAAATTCA	94
Hu.DMD.Exon46.25.011	TTTAAATCTCTTGAAATTCTGACA	95
Hu.DMD.Exon46.25.012	TGACAAGATATTCTTTGTTCTTCT	96
Hu.DMD.Exon46.25.012.2	TTCAAGTGGGATACTAGCAATGTTA	97
Hu.DMD.Exon46.25.013	AGATATTCTTTGTTCTTAGCCT	98
Hu.DMD.Exon46.25.013.2	CTGCTCTTCCAGGTTCAAGTGGG	99
Hu.DMD.Exon46.25.014	TTCTTTGTTCTTAGCCTGGAGA	100
Hu.DMD.Exon46.25.014.2	CTTTCTTTAGTTGCTGCTCTTT	101
Hu.DMD.Exon46.25.015	TTGTTCTCTAGCCTGGAGAAAGAA	102
Hu.DMD.Exon46.25.016	CTTCTAGCCTGGAGAAAGAAGAATA	103
Hu.DMD.Exon46.25.017	AGCCTGGAGAAAGAAGAATAAAATT	104
Hu.DMD.Exon46.25.018	CTGGAGAAAGAAGAATAAAATTGTT	105
Hu.DMD.Exon46.20.001	GAAAAGAAGAATAAAATTGTT	106
Hu.DMD.Exon46.20.002	GGAGAAAGAAGAATAAAATT	107
Hu.DMD.Exon46.20.003	AGCCTGGAGAAAGAAGAATA	108
Hu.DMD.Exon46.20.004	CTTCTAGCCTGGAGAAAGAA	109
Hu.DMD.Exon46.20.005	TTGTTCTCTAGCCTGGAGA	110
Hu.DMD.Exon46.20.006	TTCTTTGTTCTTAGCCT	111
Hu.DMD.Exon46.20.007	TGACAAGATATTCTTTGTT	112
Hu.DMD.Exon46.20.008	ATCTCTTGAAATTCTGACA	113
Hu.DMD.Exon46.20.009	AACAAATTCAATTAAATCTC	114
Hu.DMD.Exon46.20.010	TTCCTCCAACCATAAAACAA	115
Hu.DMD.Exon46.20.011	AGCAATGTTATCTGCTTCCT	116
Hu.DMD.Exon46.20.012	TTCAAGTGGGATACTAGCAA	117
Hu.DMD.Exon46.20.013	CTGCTCTTCCAGGTTCAA	118
Hu.DMD.Exon46.20.014	CTTTCTTTAGTTGCTGCT	119
Hu.DMD.Exon46.20.015	CTTGACTTGCTCAAGCTTT	120

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon46.20.016	ATTACCTTGACTTGCTCAAG	121
Hu.DMD.Exon46.20.017	ATAAAATTACCTTGACTTGC	122
Hu.DMD.Exon46.20.018	AGAAAATAAAATTACCTTGA	123
Hu.DMD.Exon46.20.019	ATTTGAGAAAATAAAATTAC	124
Hu.DMD.Exon46.20.020	GGGGGATTGAGAAAATAAA	125
Hu.DMD.Exon47.25.001	CTGAAACAGACAAATGCAACAACGT	126
Hu.DMD.Exon47.25.002	AGTAACTGAAACAGACAAATGCAAC	127
Hu.DMD.Exon47.25.003	CCACCAGTAACTGAAACAGACAAAT	128
Hu.DMD.Exon47.25.004	CTCTTCCACCAGTAACTGAAACAGA	129
Hu.DMD.Exon47.25.005	GGCAACTCTTCCACCAGTAACTGAA	130
Hu.DMD.Exon47.25.006	GCAGGGGCAACTCTTCCACCAGTAA	131
Hu.DMD.Exon47.25.007	CTGGCGCAGGGGCAACTCTTCCACC	132
Hu.DMD.Exon47.25.008	TTTAATTGTTGAGAATTCCCTGGCGCAGG	133
Hu.DMD.Exon47.25.008.2	TTGTTTGAGAATTCCCTGGCGCAGG	134
Hu.DMD.Exon47.25.009	GCACGGGTCCCTCCAGTTTCATTAA	135
Hu.DMD.Exon47.25.009.2	TCCAGTTCATTTAATTGTTGAGA	136
Hu.DMD.Exon47.25.010	GCTTATGGGAGCACTTACAAGCAG	137
Hu.DMD.Exon47.25.010.2	TACAAGCACGGGTCCAGTTCA	138
Hu.DMD.Exon47.25.011	AGTTTATCTTGCTCTCTGGGCTTA	139
Hu.DMD.Exon47.25.012	TCTGCTTGAGCTTATTTCAAGTT	140
Hu.DMD.Exon47.25.012.2	ATCTTGCTCTCTGGGCTTATGGGA	141
Hu.DMD.Exon47.25.013	CTTATCCACTGGAGATTGTCTGC	142
Hu.DMD.Exon47.25.013.2	CTTATTTCAAGTTATTTGCTCT	143
Hu.DMD.Exon47.25.014	CTAACCTTATCCACTGGAGATTG	144
Hu.DMD.Exon47.25.014.2	ATTTGTCTGCTTGAGCTTATTTCA	145
Hu.DMD.Exon47.25.015	AATGTCTAACCTTATCCACTGGAG	146
Hu.DMD.Exon47.25.016	TGGTTAATGTCTAACCTTATCCAC	147
Hu.DMD.Exon47.25.017	AGAGATGGTTAATGTCTAACCTTA	148
Hu.DMD.Exon47.25.018	ACGGAAGAGATGGTTAATGTCTAAC	149
Hu.DMD.Exon47.20.001	ACAGACAAATGCAACAACGT	150
Hu.DMD.Exon47.20.002	CTGAAACAGACAAATGCAAC	151
Hu.DMD.Exon47.20.003	AGTAACTGAAACAGACAAAT	152
Hu.DMD.Exon47.20.004	CCACCAGTAACTGAAACAGA	153
Hu.DMD.Exon47.20.005	CTCTTCCACCAGTAACTGAA	154
Hu.DMD.Exon47.20.006	GGCAACTCTTCCACCAGTAA	155
Hu.DMD.Exon47.20.007	CTGGCGCAGGGGCAACTCTT	156
Hu.DMD.Exon47.20.008	TTGTTTGAGAATTCCCTGGC	157

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon47.20.009	TCCAGTTCATTTAATTGTT	158
Hu.DMD.Exon47.20.010	TACAAGCACGGGTCTTCAG	159
Hu.DMD.Exon47.20.011	GCTTATGGGAGCACTTACAA	160
Hu.DMD.Exon47.20.012	ATCTTGCTCTCTGGGCTTA	161
Hu.DMD.Exon47.20.013	CTTATTTCAAGTTATCTT	162
Hu.DMD.Exon47.20.014	ATTTGTCTGCTTGAGCTTAT	163
Hu.DMD.Exon47.20.015	CTTTATCCACTGGAGATTG	164
Hu.DMD.Exon47.20.016	CTAACCTTATCCACTGGAG	165
Hu.DMD.Exon47.20.017	AATGTCTAACCTTATCCAC	166
Hu.DMD.Exon47.20.018	TGGTTAATGTCTAACCTTA	167
Hu.DMD.Exon47.20.019	AGAGATGGTTAATGTCTAAC	168
Hu.DMD.Exon47.20.020	ACGGAAGAGATGGTTAATGT	169
Hu.DMD.Exon48.25.001	CTGAAAGGAAAATACATTTAAAAA	170
Hu.DMD.Exon48.25.002	CCTGAAAGGAAAATACATTTAAAA	171
Hu.DMD.Exon48.25.002.2	GAAACCTGAAAGGAAAATACATTT	172
Hu.DMD.Exon48.25.003	GGAAACCTGAAAGGAAAATACATTT	173
Hu.DMD.Exon48.25.003.2	CTCTGGAAACCTGAAAGGAAAATAC	174
Hu.DMD.Exon48.25.004	GCTCTGGAAACCTGAAAGGAAAATA	175
Hu.DMD.Exon48.25.004.2	TAAAGCTCTGGAAACCTGAAAGGAA	634
Hu.DMD.Exon48.25.005	GTAAAGCTCTGGAAACCTGAAAGGA	176
Hu.DMD.Exon48.25.005.2	TCAGGTAAAGCTCTGGAAACCTGAA	177
Hu.DMD.Exon48.25.006	CTCAGGTAAAGCTCTGGAAACCTGA	178
Hu.DMD.Exon48.25.006.2	GTTTCTCAGGTAAAGCTCTGGAAAC	179
Hu.DMD.Exon48.25.007	TGTTTCTCAGGTAAAGCTCTGGAAA	180
Hu.DMD.Exon48.25.007.2	AATTCTCCTTGTTCTCAGGTAAA	181
Hu.DMD.Exon48.25.008	TTTGAGCTCAATTCTCCTTGTTT	182
Hu.DMD.Exon48.25.008	TTTTATTGAGCTCAATTCTCCT	183
Hu.DMD.Exon48.25.009	AAGCTGCCAAGGTCTTTATTGAA	184
Hu.DMD.Exon48.25.010	AGGTCTTCAAGCTTTTTCAAGCT	185
Hu.DMD.Exon48.25.010.2	TTCAAGCTTTTTCAAGCTGCCA	186
Hu.DMD.Exon48.25.011	GATGATTAACTGCTCTCAAGGTC	187
Hu.DMD.Exon48.25.011.2	CTGCTCTCAAGGTCTCAAGCTTT	188
Hu.DMD.Exon48.25.012	AGGAGATAACCACAGCAGCAGATGA	189
Hu.DMD.Exon48.25.012.2	CAGCAGATGATTTAACTGCTCTCA	190
Hu.DMD.Exon48.25.013	ATTCCAACGTGATTCTTAATAGGAG	191
Hu.DMD.Exon48.25.014	CTTGGTTGGTTGGTTATAAATTTC	192
Hu.DMD.Exon48.25.014.2	CAAATGATTCTAATAGGAGATAAC	193

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon48.25.015	CTTAACGTCAAATGGTCCTTCTTGG	194
Hu.DMD.Exon48.25.015.2	TTGGTTATAAATTCCAAGTGATTC	195
Hu.DMD.Exon48.25.016	CCTACCTTAACGTCAAATGGCCTT	196
Hu.DMD.Exon48.25.016.2	TCCTTCTTGGTTGGTTGGTTATAA	197
Hu.DMD.Exon48.25.017	AGTCCCTACCTTAACGTCAAATGG	198
Hu.DMD.Exon48.25.018	CAAAAAGTCCCTACCTTAACGTCA	199
Hu.DMD.Exon48.25.019	TAAAGCAAAAAGTCCCTACCTTAA	200
Hu.DMD.Exon48.25.020	ATATTAAAGCAAAAAGTCCCTAC	201
Hu.DMD.Exon48.20.001	AGGAAAATACATTTAAAAAA	202
Hu.DMD.Exon48.20.002	AAGGAAAATACATTTAAAAAA	203
Hu.DMD.Exon48.20.003	CCTGAAAGGAAAATACATTT	204
Hu.DMD.Exon48.20.004	GGAACCTGAAAGGAAAATA	205
Hu.DMD.Exon48.20.005	GCTCTGGAAACCTGAAAGGA	206
Hu.DMD.Exon48.20.006	GTAAAGCTCTGGAAACCTGA	207
Hu.DMD.Exon48.20.007	CTCAGGTAAAGCTCTGGAAA	208
Hu.DMD.Exon48.20.008	AATTCTCCTTGTGTTCTCAG	209
Hu.DMD.Exon48.20.009	TTTTATTGAGCTTCATT	210
Hu.DMD.Exon48.20.010	AAGCTGCCAAGGTCTTTA	211
Hu.DMD.Exon48.20.011	TTCAAGCTTTTTCAAGCT	212
Hu.DMD.Exon48.20.012	CTGCTCTCAAGGTCTTCAA	213
Hu.DMD.Exon48.20.013	CAGCAGATGATTAACTGCT	214
Hu.DMD.Exon48.20.014	AGGAGATAACCACAGCAGCA	215
Hu.DMD.Exon48.20.015	CAACTGATTCTAAATAGGAG	216
Hu.DMD.Exon48.20.016	TTGGTTATAAATTCCAAGT	217
Hu.DMD.Exon48.20.017	TCCTTCTTGGTTGGTTGGT	218
Hu.DMD.Exon48.20.018	CTTAACGTCAAATGGCCTT	219
Hu.DMD.Exon48.20.019	CCTACCTTAACGTCAAATGG	220
Hu.DMD.Exon48.20.020	AGTCCCTACCTTAACGTCA	221
Hu.DMD.Exon48.20.021	CAAAAAGTCCCTACCTTAA	222
Hu.DMD.Exon48.20.022	TAAAGCAAAAAGTCCCTAC	223
Hu.DMD.Exon48.20.023	ATATTAAAGCAAAAAGTTC	224
Hu.DMD.Exon49.25.001	CTGGGGAAAAGAACCCATATAGTGC	225
Hu.DMD.Exon49.25.002	TCCTGGGGAAAAGAACCCATATAGT	226
Hu.DMD.Exon49.25.002.2	TTTCCTGGGGAAAAGAACCCATAT	227
Hu.DMD.Exon49.25.003	CAGTTCTGGGGAAAAGAACCCAT	228
Hu.DMD.Exon49.25.003.2	TTTCAGTTCTGGGGAAAAGAAC	229
Hu.DMD.Exon49.25.004	TATTCAGTTCTGGGGAAAAGAA	230

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon49.25.004.2	TGCTATTTCAGTTCCCTGGGGAAAA	231
Hu.DMD.Exon49.25.005	ACTGCTATTCAGTTCTGGGGAA	232
Hu.DMD.Exon49.25.005.2	TGAAC TGCTATTCAGTTCCCTGGG	233
Hu.DMD.Exon49.25.006	CTTGAAC TGCTATTCAGTTCCCTG	234
Hu.DMD.Exon49.25.006.2	TAGCTTGAACTGCTATTCAGTTTC	235
Hu.DMD.Exon49.25.007	TTTAGCTTGAACTGCTATTCAGTT	236
Hu.DMD.Exon49.25.008	TTCCACACATCCGGTTGTTAGCTTGA	237
Hu.DMD.Exon49.25.009	TGCCCTTAGACAAAATCTCTTCCA	238
Hu.DMD.Exon49.25.009.2	TTTAGACAAAATCTCTTCCACATCC	239
Hu.DMD.Exon49.25.010	GTTTTCCCTGTACAAATGCTGCC	240
Hu.DMD.Exon49.25.010.2	GTACAAATGCTGCCCTTAGACAAA	241
Hu.DMD.Exon49.25.011	CTTCACTGGCTGAGTGGCTGGTTT	242
Hu.DMD.Exon49.25.011.2	GGCTGGTTTTCCTGTACAAATGC	243
Hu.DMD.Exon49.25.012	ATTACCTCACTGGCTGAGTGGCTG	244
Hu.DMD.Exon49.25.013	GCTTCATTACCTTCACTGGCTGAGT	245
Hu.DMD.Exon49.25.014	AGGTTGCTTCATTACCTTCACTGGC	246
Hu.DMD.Exon49.25.015	GCTAGAGGTTGCTTCATTACCTTCA	247
Hu.DMD.Exon49.25.016	ATATTGCTAGAGGTTGCTTCATTAC	248
Hu.DMD.Exon49.20.001	GAAAAGAACCCATATAAGTGC	249
Hu.DMD.Exon49.20.002	GGGAAAAGAACCCATATAAGT	250
Hu.DMD.Exon49.20.003	TCCTGGGAAAAGAACCCAT	251
Hu.DMD.Exon49.20.004	CAGTTCCCTGGGGAAAAGAA	252
Hu.DMD.Exon49.20.005	TATTCAGTTCCCTGGGGAA	253
Hu.DMD.Exon49.20.006	ACTGCTATTCAGTTCCCTG	254
Hu.DMD.Exon49.20.007	CTTGAAC TGCTATTCAGTT	255
Hu.DMD.Exon49.20.008	TTTAGCTTGAACTGCTATT	256
Hu.DMD.Exon49.20.009	TTCCACACATCCGGTTGTTAG	257
Hu.DMD.Exon49.20.010	TTTAGACAAAATCTCTTCCA	258
Hu.DMD.Exon49.20.011	GTACAAATGCTGCCCTTAG	259
Hu.DMD.Exon49.20.012	GGCTGGTTTTCCTGTACA	260
Hu.DMD.Exon49.20.013	CTTCACTGGCTGAGTGGCTG	261
Hu.DMD.Exon49.20.014	ATTACCTCACTGGCTGAGT	262
Hu.DMD.Exon49.20.015	GCTTCATTACCTTCACTGGC	263
Hu.DMD.Exon49.20.016	AGGTTGCTTCATTACCTTCA	264
Hu.DMD.Exon49.20.017	GCTAGAGGTTGCTTCATTAC	265
Hu.DMD.Exon49.20.018	ATATTGCTAGAGGTTGCTTC	266
Hu.DMD.Exon50.25.001	CTTTAACAGAAAAGCATACACATTA	267

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon50.25.002	TCCTCTTTAACAGAAAAGCATAAC	268
Hu.DMD.Exon50.25.002.2	TTCCCTCTTTAACAGAAAAGCATAAC	269
Hu.DMD.Exon50.25.003	TAACCTCCCTTTAACAGAAAAGCA	270
Hu.DMD.Exon50.25.003.2	CTAAACTCCTCTTTAACAGAAAAGC	271
Hu.DMD.Exon50.25.004	TCTTCTAACTTCCTCTTTAACAGAA	272
Hu.DMD.Exon50.25.004.2	ATCTTCTAACTTCCTCTTTAACAGA	273
Hu.DMD.Exon50.25.005	TCAGATCTCTAACTTCCTCTTTAA	274
Hu.DMD.Exon50.25.005.2	CTCAGATCTCTAACTTCCTCTTTA	275
Hu.DMD.Exon50.25.006	AGAGCTCAGATCTCTAACTTCCTC	276
Hu.DMD.Exon50.25.006.2	CAGAGCTCAGATCTCTAACTTCCT NG-08-0731	277
Hu.DMD.Exon50.25.007	CACTCAGAGCTCAGATCTCTACT	278
Hu.DMD.Exon50.25.007.2	CCTTCCACTCAGAGCTCAGATCTTC	279
Hu.DMD.Exon50.25.008	GTAAACGGTTTACCGCCTTCCACTC	280
Hu.DMD.Exon50.25.009	CTTGCCCTCAGCTCTTGAAGTAAA	281
Hu.DMD.Exon50.25.009.2	CCCTCAGCTCTTGAAGTAAACGGTT	282
Hu.DMD.Exon50.25.010	CCAGGAGCTAGGTCAGGCTGTTG	283
Hu.DMD.Exon50.25.010.2	GGTCAGGCTGCTTGCCCTCAGCTC	284
Hu.DMD.Exon50.25.011	AGGCTCCAATAGTGGTCAGTCCAGG	285
Hu.DMD.Exon50.25.011.2	TCAGTCCAGGAGCTAGGTAGGCTCAG	286
Hu.DMD.Exon50.25.012	CTTACAGGCTCCAATAGTGGTCAGT AVI-5038	287
Hu.DMD.Exon50.25.013	GTATACTTACAGGCTCCAATAGTGG	288
Hu.DMD.Exon50.25.014	ATCCAGTATACTTACAGGCTCCAAT	289
Hu.DMD.Exon50.25.015	ATGGGATCCAGTATACTTACAGGCT NG-08-0741	290
Hu.DMD.Exon50.25.016	AGAGAATGGGATCCAGTATACTTAC NG-08-0742	291
Hu.DMD.Exon50.20.001	ACAGAAAAGCATACACATTA	292
Hu.DMD.Exon50.20.002	TTAACAGAAAAGCATAACAC	293
Hu.DMD.Exon50.20.003	TCCTCTTTAACAGAAAAGCA	294
Hu.DMD.Exon50.20.004	TAACCTCCCTTTAACAGAA	295
Hu.DMD.Exon50.20.005	TCTTCTAACTTCCTCTTTAA	296
Hu.DMD.Exon50.20.006	TCAGATCTCTAACTTCCTC	297
Hu.DMD.Exon50.20.007	CCTTCCACTCAGAGCTCAGA	298
Hu.DMD.Exon50.20.008	GTAAACGGTTTACCGCCTTC	299
Hu.DMD.Exon50.20.009	CCCTCAGCTCTTGAAGTAAA	300
Hu.DMD.Exon50.20.010	GGTCAGGCTGCTTGCCCTC	301
Hu.DMD.Exon50.20.011	TCAGTCCAGGAGCTAGGTCA	302

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon50.20.012	AGGCTCCAATAGTGGTCAGT	303
Hu.DMD.Exon50.20.013	CTTACAGGCTCCAATAGTGG	304
Hu.DMD.Exon50.20.014	GTATACTTACAGGCTCCAAT	305
Hu.DMD.Exon50.20.015	ATCCAGTATACTTACAGGCT	306
Hu.DMD.Exon50.20.016	ATGGGATCCAGTATACTTAC	307
Hu.DMD.Exon50.20.017	AGAGAATGGGATCCAGTATA	308
Hu.DMD.Exon51.25.001-44	CTAAAATTTGGGTTTGCAAA	309
Hu.DMD.Exon51.25.002-45	GCTAAAATTTGGGTTTGCAAA	310
Hu.DMD.Exon51.25.002-2-46	TAGGAGCTAAAATTTGGGTTTT	311
Hu.DMD.Exon51.25.003	AGTAGGAGCTAAAATTTGGGTT	312
Hu.DMD.Exon51.25.003.2	TGAGTAGGAGCTAAAATTTGGG	313
Hu.DMD.Exon51.25.004	CTGAGTAGGAGCTAAAATTTGGG	314
Hu.DMD.Exon51.25.004.2	CAGTCTGAGTAGGAGCTAAAATATT	315
Hu.DMD.Exon51.25.005	ACAGTCTGAGTAGGAGCTAAAATATT	316
Hu.DMD.Exon51.25.005.2	GAGTAACAGTCTGAGTAGGAGCTAAA	317
Hu.DMD.Exon51.25.006	CAGAGTAACAGTCTGAGTAGGAGCT	318
Hu.DMD.Exon51.25.006.2	CACCAGAGTAACAGTCTGAGTAGGAG	319
Hu.DMD.Exon51.25.007	GTCACCAGAGTAACAGTCTGAGTAG	320
Hu.DMD.Exon51.25.007.2	AACCACAGGTTGTGTCAACCAGAGTAA	321
Hu.DMD.Exon51.25.008	GTTGTGTCAACCAGAGTAACAGTCTG	322
Hu.DMD.Exon51.25.009	TGGCAGTTCCCTAGTAACCACAGGT	323
Hu.DMD.Exon51.25.010	ATTCTAGTTGGAGATGGCAGTTTC	324
Hu.DMD.Exon51.25.010.2	GGAAGATGGCATTCTAGTTGGAG	325
Hu.DMD.Exon51.25.011	CATCAAGGAAGATGGCATTCTAGTT	326
Hu.DMD.Exon51.25.011.2	GAGCAGGTACCTCCAACATCAAGGAA	327
Hu.DMD.Exon51.25.012	ATCTGCCAGAGCAGGTACCTCCAAC	328
Hu.DMD.Exon51.25.013	AAGTTCTGTCCAAGCCCCGGTTGAAAT	329
Hu.DMD.Exon51.25.013.2	CGGTTGAAATCTGCCAGAGCAGGTAC	330
Hu.DMD.Exon51.25.014	GAGAAAGCCAGTCGGTAAGTTCTGTC	331
Hu.DMD.Exon51.25.014.2	GTCGGTAAGTTCTGTCCAAGCCCGG	332
Hu.DMD.Exon51.25.015	ATAACTTGATCAAGCAGAGAAAGCCA	333
Hu.DMD.Exon51.25.015.2	AAGCAGAGAAAGCCAGTCGGTAAGT	334
Hu.DMD.Exon51.25.016	CACCCTCTGTGATTTATAACTTGAT	335
Hu.DMD.Exon51.25.017	CAAGGTACCCACCACCATCACCTCTGT	336
Hu.DMD.Exon51.25.017.2	CATCACCCCTGTGATTTATAACT	337
Hu.DMD.Exon51.25.018	CTTCTGCTTGATGATCATCTCGTTGA	338

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon51.25.019	CCTTCTGCTTGATGATCATCTCGTTG	339
Hu.DMD.Exon51.25.019.2	ATCTCGTTGATATCCTCAAGGTACCC	340
Hu.DMD.Exon51.25.020	TCATACCTTCTGCTTGATGATCATCT	341
Hu.DMD.Exon51.25.020.2	TCATTTTTCTCATACCTTCTGCTTG	342
Hu.DMD.Exon51.25.021	TTTTCTCATACCTTCTGCTTGATGAT	343
Hu.DMD.Exon51.25.022	TTTTATCATTTTCTCATACCTTCT	344
Hu.DMD.Exon51.25.023	CCAACCTTTATCATTTTCTCATAC	345
Hu.DMD.Exon51.20.001	ATATTTGGGTTTTGAAA	346
Hu.DMD.Exon51.20.002	AAAATATTTGGGTTTTGC	347
Hu.DMD.Exon51.20.003	GAGCTAAATATTTGGGTT	348
Hu.DMD.Exon51.20.004	AGTAGGAGCTAAATATTT	349
Hu.DMD.Exon51.20.005	GTC TGAGTAGGAGCTAAAT	350
Hu.DMD.Exon51.20.006	TAACAGTCTGAGTAGGAGCT	351
Hu.DMD.Exon51.20.007	CAGAGTAACAGTCTGAGTAG	352
Hu.DMD.Exon51.20.008	CACAGGTTGTCACCAGAG	353
Hu.DMD.Exon51.20.009	AGTTCCCTAGTAACCACAG	354
Hu.DMD.Exon51.20.010	TAGTTGGAGATGGCAGTT	355
Hu.DMD.Exon51.20.011	GGAAGATGGCATTCTAGTT	356
Hu.DMD.Exon51.20.012	TACCTCCAACATCAAGGAAG	357
Hu.DMD.Exon51.20.013	ATCTGCCAGAGCAGGTACCT	358
Hu.DMD.Exon51.20.014	CCAAGCCCCGTTGAAATCTG	359
Hu.DMD.Exon51.20.015	GTCGGTAAGTTCTGTCCAAG	360
Hu.DMD.Exon51.20.016	AAGCAGAGAAAGCCAGTCGG	361
Hu.DMD.Exon51.20.017	TTTTATAACTGATCAAGCA	362
Hu.DMD.Exon51.20.018	CATCACCCCTCTGTGATTTA	363
Hu.DMD.Exon51.20.019	CTCAAGGTCACCCACCATCA	364
Hu.DMD.Exon51.20.020	CATCTCGTTGATATCCTCAA	365
Hu.DMD.Exon51.20.021	CTTCTGCTTGATGATCATCT	366
Hu.DMD.Exon51.20.022	CATACCTTCTGCTTGATGAT	367
Hu.DMD.Exon51.20.023	TTTCTCATACCTTCTGCTTG	368
Hu.DMD.Exon51.20.024	CATTTTTCTCATACCTTCT	369
Hu.DMD.Exon51.20.025	TTTATCATTTTCTCATAC	370
Hu.DMD.Exon51.20.026	CAACTTTATCATTTTCT	371
Hu.DMD.Exon52.25.001	CTGTAAGAACAAATATCCCTTAGTA	372
Hu.DMD.Exon52.25.002	TGCCTGTAAGAACAAATATCCCTTA	373
Hu.DMD.Exon52.25.002.2	GTTGCCTGTAAGAACAAATATCCCT	374
Hu.DMD.Exon52.25.003	ATTGTTGCCTGTAAGAACAAATATC	375

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon52.25.003.2	GCATTGTTGCCCTGTAAGAACAAATA	376
Hu.DMD.Exon52.25.004	CCTGCATTGTTGCCCTGTAAGAACAA	377
Hu.DMD.Exon52.25.004.2	ATCCTGCATTGTTGCCCTGTAAGAAC	378
Hu.DMD.Exon52.25.005	CAAATCCTGCATTGTTGCCCTGTAAG	379
Hu.DMD.Exon52.25.005.2	TCCAAATCCTGCATTGTTGCCCTGTA	380
Hu.DMD.Exon52.25.006	TGTTCCAATCCTGCATTGTTGCCT	381
Hu.DMD.Exon52.25.006.2	TCTGTTCCAAATCCTGCATTGTTGC	382
Hu.DMD.Exon52.25.007	AACTGGGGACGCCCTGTTCCAAAT	383
Hu.DMD.Exon52.25.007.2	GCCTCTGTTCCAAATCCTGCATTGT	384
Hu.DMD.Exon52.25.008	CAGCGGTAATGAGTTCTTCAACTG	385
Hu.DMD.Exon52.25.008.2	CTTCCAAC TG GGG AC GC CT CT GT TC	386
Hu.DMD.Exon52.25.009	CTTGTTTTCAAATTTGGG CAG CG	387
Hu.DMD.Exon52.25.010	CTAGCCTCTTGATTGCTGGTCTTGT	388
Hu.DMD.Exon52.25.010.2	TTTCAAAATTTGGG CAG CG GT AA	389
Hu.DMD.Exon52.25.011	TTCGATCCGTAATGATTGTTCTAGC	390
Hu.DMD.Exon52.25.011.2	GATTGCTGGTCTTGTTTTCAAATT	391
Hu.DMD.Exon52.25.012	CTTACTTCGATCCGTAATGATTGTT	392
Hu.DMD.Exon52.25.012.2	TTGTTCTAGCCTCTGATTGCTGGT	393
Hu.DMD.Exon52.25.013	AAAAACTTACTTCGATCCGTAATGA	394
Hu.DMD.Exon52.25.014	TGTTAAAAAAACTTACTTCGATCCGT	395
Hu.DMD.Exon52.25.015	ATGCTTGTTAAAAAAACTTACTTCGA	396
Hu.DMD.Exon52.25.016	GTCCC ATGCTTGT TAAAAAAACTTAC	397
Hu.DMD.Exon52.20.001	AGAACAAATATCCCTTAGTA	398
Hu.DMD.Exon52.20.002	GTAAGAACAAATATCCCTTA	399
Hu.DMD.Exon52.20.003	TGCCTGTAAGAACAAATATC	400
Hu.DMD.Exon52.20.004	ATTGTTGCCCTGTAAGAACAA	401
Hu.DMD.Exon52.20.005	CCTGCATTGTTGCCCTGTAAG	402
Hu.DMD.Exon52.20.006	CAAATCCTGCATTGTTGCCT	403
Hu.DMD.Exon52.20.007	GCCTCTGTTCCAAATCCTGC	404
Hu.DMD.Exon52.20.008	CTTCCAAC TG GGG AC GC CT C	405
Hu.DMD.Exon52.20.009	CAGCGGTAATGAGTTCTTCC	406
Hu.DMD.Exon52.20.010	TTTCAAAATTTGGG CAG CG	407
Hu.DMD.Exon52.20.011	GATTGCTGGTCTTGTTTTTC	408
Hu.DMD.Exon52.20.012	TTGTTCTAGCCTCTGATTG	409
Hu.DMD.Exon52.20.013	TTCGATCCGTAATGATTGTT	410
Hu.DMD.Exon52.20.014	CTTACTTCGATCCGTAATGA	411
Hu.DMD.Exon52.20.015	AAAAACTTACTTCGATCCGT	412

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon52.20.016	TGTTAAAAAACTTACTTCGA	413
Hu.DMD.Exon52.20.017	ATGCTTGTTAAAAAACTTAC	414
Hu.DMD.Exon52.20.018	GTCcccATGCTTGTAAAAAA	415
Hu.DMD.Exon53.25.001	CTAGAATAAAAGGAAAAATAAAATAT	416
Hu.DMD.Exon53.25.002	AACTAGAATAAAAGGAAAAATAAAAT	417
Hu.DMD.Exon53.25.002.2	TTCAACTAGAATAAAAGGAAAAATA	418
Hu.DMD.Exon53.25.003	CTTTCAACTAGAATAAAAGGAAAAAA	419
Hu.DMD.Exon53.25.003.2	ATTCTTCAACTAGAATAAAAGGAA	420
Hu.DMD.Exon53.25.004	GAATTCTTCAACTAGAATAAAAGG	421
Hu.DMD.Exon53.25.004.2	TCTGAATTCTTCAACTAGAATAAA	422
Hu.DMD.Exon53.25.005	ATTCTGAATTCTTCAACTAGAATA	423
Hu.DMD.Exon53.25.005.2	CTGATTCTGAATTCTTCAACTAGA	424
Hu.DMD.Exon53.25.006	CACTGATTCTGAATTCTTCAACTA	425
Hu.DMD.Exon53.25.006.2	TCCCAC TGATTCTGAATTCTTCAA	426
Hu.DMD.Exon53.25.007	CATCCCAC TGATTCTGAATTCTTC	427
Hu.DMD.Exon53.25.008	TACTTCATCCCAC TGATTCTGAATT	428
Hu.DMD.Exon53.25.008.2	CTGAAGGTGTTCTTGTACTTCATCC	429
Hu.DMD.Exon53.25.009	CGGTTCTGAAGGTGTTCTTGTACT	430
Hu.DMD.Exon53.25.009.2	CTGTTGCCTCCGGTTCTGAAGGTGT	431
Hu.DMD.Exon53.25.010	TTTCATTCAACTGTTGCCTCCGGTT	432
Hu.DMD.Exon53.25.010.2	TAACATTTCAATTCAACTGTTGCCTC	433
Hu.DMD.Exon53.25.011	TTGTGTTGAATCCTTAAACATTCA	434
Hu.DMD.Exon53.25.012	TCTTCCTTAGCTTCCAGGCCATTGTG	435
Hu.DMD.Exon53.25.012.2	CTTAGCTTCCAGGCCATTGTGTTGAA	436
Hu.DMD.Exon53.25.013	GTCCTTAAGACCTGCTCAGCTTCTC	437
Hu.DMD.Exon53.25.013.2	CTGCTCAGCTTCTTCCATTGCTTCC	438
Hu.DMD.Exon53.25.014	CTCAAGCTTGGCTCTGGCTGTCT	439
Hu.DMD.Exon53.25.014.2	GGCCTGTCCTAACGACCTGCTCAGCT	440
Hu.DMD.Exon53.25.015	TAGGGACCCCTCCTCCATTGACTCAA	441
Hu.DMD.Exon53.25.016	TTTGGATTGCATCTACTGTATAGGG	442
Hu.DMD.Exon53.25.016.2	ACCCTCCTCCATTGACTAACGCTTG	443
Hu.DMD.Exon53.25.017	CTTGGTTCTGTGATTTCTTTGG	444
Hu.DMD.Exon53.25.017.2	ATCTACTGTATAGGGACCCCTCCTC	445
Hu.DMD.Exon53.25.018	CTAACCTGGTTCTGTGATTTCT	446
Hu.DMD.Exon53.25.018.2	TTTCTTTGGATTGCATCTACTGTA	447
Hu.DMD.Exon53.25.019	TGATACTAACCTGGTTCTGTGAT	448
Hu.DMD.Exon53.25.020	ATCTTGATACTAACCTGGTTCT	449

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon53.25.021	AAGGTATCTTGATACTAACCTTGG	450
Hu.DMD.Exon53.25.022	TTAAAAAGGTATCTTGATACTAAC	451
Hu.DMD.Exon53.20.001	ATAAAAGGAAAAATAAATAT	452
Hu.DMD.Exon53.20.002	GAATAAAAGGAAAAATAAAT	453
Hu.DMD.Exon53.20.003	AACTAGAATAAAAGGAAAAA	454
Hu.DMD.Exon53.20.004	CTTTCAACTAGAATAAAGG	455
Hu.DMD.Exon53.20.005	GAATTCTTCAACTAGAATA	456
Hu.DMD.Exon53.20.006	ATTCTGAATTCTTCAACTA	457
Hu.DMD.Exon53.20.007	TACTTCATCCCACTGATTCT	458
Hu.DMD.Exon53.20.008	CTGAAGGTGTTCTTGTACT	459
Hu.DMD.Exon53.20.009	CTGTTGCCTCCGGTCTGAA	460
Hu.DMD.Exon53.20.010	TAACATTCATTCAACTGTT	461
Hu.DMD.Exon53.20.011	TTGTGTTGAATCCTTTAAC	462
Hu.DMD.Exon53.20.012	CTTAGCTTCCAGCCATTGTG	463
Hu.DMD.Exon53.20.013	CTGCTCAGCTTCTCCCTAG	464
Hu.DMD.Exon53.20.014	GGCCTGTCTTAAGACCTGCT	465
Hu.DMD.Exon53.20.015	CTCAAGCTTGGCTCTGGCCT	466
Hu.DMD.Exon53.20.016	ACCCCTCCTCCATGACTCAA	467
Hu.DMD.Exon53.20.017	ATCTACTGTATAGGGACCT	468
Hu.DMD.Exon53.20.018	TTTCTTTGGATTGCATCTA	469
Hu.DMD.Exon53.20.019	CTTGGTTCTGTGATTTCT	470
Hu.DMD.Exon53.20.020	CTAACCTTGGTTCTGTGAT	471
Hu.DMD.Exon53.20.021	TGATACTAACCTTGGTTCT	472
Hu.DMD.Exon53.20.022	ATCTTGATACTAACCTTGG	473
Hu.DMD.Exon53.20.023	AAGGTATCTTGATACTAAC	474
Hu.DMD.Exon53.20.024	TTAAAAAGGTATCTTGATA	475
Hu.DMD.Exon54.25.001	CTATAGATTTCATGAGAAAGAGA	476
Hu.DMD.Exon54.25.002	AACTGCTATAGATTTTATGAGAAA	477
Hu.DMD.Exon54.25.003	TGGCCAAGTGTATAGATTTTATG	478
Hu.DMD.Exon54.25.004	GTCTTGCCAACTGCTATAGATT	479
Hu.DMD.Exon54.25.005	CGGAGGTCTTGGCCAAGTGTATA	480
Hu.DMD.Exon54.25.006	ACTGGCGGAGGTCTTGGCCAAGTG	481
Hu.DMD.Exon54.25.007	TTTGTCTGCCACTGGCGGAGGTCTT	482
Hu.DMD.Exon54.25.008	AGTCATTGCCACATCTACATTGT	483
Hu.DMD.Exon54.25.008.2	TTTGCCACATCTACATTGTCTGCC	484
Hu.DMD.Exon54.25.009	CCGGAGAAGTTCAAGGGCAAGTCA	485
Hu.DMD.Exon54.25.010	GTATCATCTGCAGAATAATCCCGGA	486

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon54.25.010.2	TAATCCGGAGAAGTTCAGGGCCA	487
Hu.DMD.Exon54.25.011	TTATCATGTGGACTTTCTGGTATC	488
Hu.DMD.Exon54.25.012	AGAGGCATTGATATTCTCTGTTATC	489
Hu.DMD.Exon54.25.012.2	ATGTGGACTTTCTGGTATCATCTG	490
Hu.DMD.Exon54.25.013	CTTTTATGAATGCTTCTCCAAGAGG	491
Hu.DMD.Exon54.25.013.2	ATATTCTCTGTTATCATGTGGACTT	492
Hu.DMD.Exon54.25.014	CATACCTTTATGAATGCTTCTCCA	493
Hu.DMD.Exon54.25.014.2	CTCCAAGAGGCATTGATATTCTCTG	494
Hu.DMD.Exon54.25.015	TAATTACATACCTTTATGAATGCTT	495
Hu.DMD.Exon54.25.015.2	CTTTTATGAATGCTTCTCCAAGAGG	496
Hu.DMD.Exon54.25.016	TAATGTAATTACACCTTTATGAA	497
Hu.DMD.Exon54.25.017	AGAAAATAATGTAATTACACCTTT	498
Hu.DMD.Exon54.25.018	GTTTTAGAAATAATGTAATTACAC	499
Hu.DMD.Exon54.20.001	GATTTTATGAGAAAGAGA	500
Hu.DMD.Exon54.20.002	CTATAGATTTTATGAGAAA	501
Hu.DMD.Exon54.20.003	AACTGCTATAGATTTTATG	502
Hu.DMD.Exon54.20.004	TGGCCAAGTGCTATAGATT	503
Hu.DMD.Exon54.20.005	GTCTTGCCAACTGCTATA	504
Hu.DMD.Exon54.20.006	CGGAGGTCTTGGCCAAGTG	505
Hu.DMD.Exon54.20.007	TTTGTCTGCCACTGGCGGAG	506
Hu.DMD.Exon54.20.008	TTTGCCACATCTACATTTGT	507
Hu.DMD.Exon54.20.009	TTCAAGGGCCAAGTCATTGC	508
Hu.DMD.Exon54.20.010	TAATCCGGAGAAGTTCAG	509
Hu.DMD.Exon54.20.011	GTATCATCTGCAGAATAATC	510
Hu.DMD.Exon54.20.012	ATGTGGACTTTCTGGTATC	511
Hu.DMD.Exon54.20.013	ATATTCTCTGTTATCATGTG	512
Hu.DMD.Exon54.20.014	CTCCAAGAGGCATTGATATT	513
Hu.DMD.Exon54.20.015	CTTTTATGAATGCTTCTCCA	514
Hu.DMD.Exon54.20.016	CATACCTTTATGAATGCTT	515
Hu.DMD.Exon54.20.017	TAATTACATACCTTTATGAA	516
Hu.DMD.Exon54.20.018	TAATGTAATTACACCTTT	517
Hu.DMD.Exon54.20.019	AGAAAATAATGTAATTACAC	518
Hu.DMD.Exon54.20.020	GTTTTAGAAATAATGTAATT	519
Hu.DMD.Exon55.25.001	CTGCAAAGGACCAAATGTCAGATG	520
Hu.DMD.Exon55.25.002	TCACCCCTGCAAAGGACCAAATGTC	521
Hu.DMD.Exon55.25.003	CTCACTCACCCCTGCAAAGGACCAA	522
Hu.DMD.Exon55.25.004	TCTCGCTCACTCACCCCTGCAAAGGA	523

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon55.25.005	CAGCCTCTCGCTCACTCACCCCTGCA	524
Hu.DMD.Exon55.25.006	CAAAGCAGCCTCTCGCTCACTCACC	525
Hu.DMD.Exon55.25.007	TCTTCCAAGCAGCCTCTCGCTCAC	526
Hu.DMD.Exon55.25.007.2	TCTATGAGTTTCTTCCAAGCAGCC	527
Hu.DMD.Exon55.25.008	GTTGCAGTAATCTATGAGTTTCTTC	528
Hu.DMD.Exon55.25.008.2	GAACTGTTGCAGTAATCTATGAGTT	529
Hu.DMD.Exon55.25.009	TTCCAGGTCCAGGGGGAACTGTTGC	530
Hu.DMD.Exon55.25.010	GTAAGCCAGGCAAGAAACTTTCCA	531
Hu.DMD.Exon55.25.010.2	CCAGGCAAGAAACTTTCCAGGTCC	532
Hu.DMD.Exon55.25.011	TGGCAGTTGTTTCAGCTCTGTAAG	533
Hu.DMD.Exon55.25.011.2	TTCAGCTTCTGTAAGCCAGGCAAGA	635
Hu.DMD.Exon55.25.012	GGTAGCATCCTGTAGGACATTGGCA	534
Hu.DMD.Exon55.25.012.2	GACATTGGCAGTTGTTTCAGCTTCT	535
Hu.DMD.Exon55.25.013	TCTAGGAGCCTTCCCTAACGGTAG	536
Hu.DMD.Exon55.25.014	CTTTTACTCCCTTGAGTCTTCTAG	537
Hu.DMD.Exon55.25.014.2	GAGCCTTCCTTACGGTAGCATCC	538
Hu.DMD.Exon55.25.015	TTGCCATTGTTTCATCAGCTTTTT	539
Hu.DMD.Exon55.25.015.2	CTTGGAGTCTTCTAGGAGCCTTCC	540
Hu.DMD.Exon55.25.016	CTTACTTGCCATTGTTTCATCAGCT	541
Hu.DMD.Exon55.25.016.2	CAGCTCTTTACTCCCTGGAGTCT	542
Hu.DMD.Exon55.25.017	CCTGACTTACTTGCCATTGTTCAT	543
Hu.DMD.Exon55.25.018	AAATGCCTGACTTACTTGCCATTGT	544
Hu.DMD.Exon55.25.019	AGCGGAATGCCTGACTTACTTGCC	545
Hu.DMD.Exon55.25.020	GCTAAAGCGGAATGCCTGACTTAC	546
Hu.DMD.Exon55.20.001	AAGGACCAAATGTTCAGATG	547
Hu.DMD.Exon55.20.002	CTGCAAAGGACCAAATGTT	548
Hu.DMD.Exon55.20.003	TCACCCCTGCAAAGGACAAA	549
Hu.DMD.Exon55.20.004	CTCACTCACCCCTGCAAAGGA	550
Hu.DMD.Exon55.20.005	TCTCGCTCACTCACCCCTGCA	551
Hu.DMD.Exon55.20.006	CAGCCTCTCGCTCACTCACC	552
Hu.DMD.Exon55.20.007	CAAAGCAGCCTCTCGCTCAC	553
Hu.DMD.Exon55.20.008	TCTATGAGTTTCTTCCAAG	554
Hu.DMD.Exon55.20.009	GAACTGTTGCAGTAATCTAT	555
Hu.DMD.Exon55.20.010	TTCCAGGTCCAGGGGGAACT	556
Hu.DMD.Exon55.20.011	CCAGGCAAGAAACTTTCCA	557
Hu.DMD.Exon55.20.012	TTCAGCTTCTGTAAGCCAGG	558
Hu.DMD.Exon55.20.013	GACATTGGCAGTTGTTTCAG	559

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Name	Sequences	SEQ ID NO.
Hu.DMD.Exon55.20.014	GGTAGCATCCTGTTAGGACAT	560
Hu.DMD.Exon55.20.015	GAGCCTTCCTTACGGGTAG	561
Hu.DMD.Exon55.20.016	CTTGGAGTCTTCTAGGAGCC	562
Hu.DMD.Exon55.20.017	CAGCTCTTTACTCCCTGG	563
Hu.DMD.Exon55.20.018	TTGCCATTGTTTCATCAGCT	564
Hu.DMD.Exon55.20.019	CTTACTTGCCATTGTTTCAT	565
Hu.DMD.Exon55.20.020	CCTGACTTACTTGCCATTGT	566
Hu.DMD.Exon55.20.021	AAATGCCTGACTTACTTGCC	567
Hu.DMD.Exon55.20.022	AGCGGAAATGCCTGACTTAC	568
Hu.DMD.Exon55.20.023	GCTAAAGCGGAAATGCCTGA	569
H50A(+02+30)-AVI-5656	CCACTCAGAGCTCAGATCTTCTAACTTCC	584
H50D(+07-18)-AVI-5915	GGGATCCAGTATACTTACAGGCTCC	585
H50A(+07+33)	CTTCCACTCAGAGCTCAGATCTTCTAA	586
H51A(+61+90)-AVI-4657	ACATCAAGGAAGATGGCATTCTAGTTGG	587
H51A(+66+95)-AVI-4658	CTCCAACATCAAGGAAGATGGCATTCTAG	588
H51A(+111+134)	TTCTGTCCAAGCCCGGTTGAAATC	589
H51A(+175+195)	CACCCACCACATCACCCCTYGTG	590
H51A(+199+220)	ATCATCTCGTTGATATCCTCAA	591
H51A(+66+90)	ACATCAAGGAAGATGGCATTCTAG	592
H51A(-01+25)	ACCAGAGTAACAGTCTGAGTAGGAGC	593
h51AON1	TCAAGGAAGATGGCATTCT	594
h51AON2	CCTCTGTGATTTTATAACCTGAT	595
H51D(+08-17)	ATCATTTTCTCATACCTCTGCT	596
H51D(+16-07)	CTCATACCTCTGCTTGATGATC	597
hAON#23	TGGCATTCTAGTTGG	598
hAON#24	CCAGAGCAGGTACCTCAACATC	599
H44A(+61+84)	TGTTCAGCTTCTGTTAGCCACTGA	600
H44A(+85+104)	TTTGTGTCTTCTGAGAAC	601
h44AON1	CGCCGCCATTCTCAACAG	602
H44A(-06+14)	ATCTGTCAAATGCCTGAG	603
H45A(+71+90)	TGTTTTGAGGATTGCTGAA	604
h45AON1	GCTGAATTATTCTTCCCC	605
h45AON5	GCCCAATGCCATCCTGG	606
H45A(-06+20)	CCAATGCCATCCTGGAGTTCTGTAA	607
H53A(+39+69)	CATTCAACTGTTGCCTCCGGTTCTGAAGGTG	608

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Name	Sequences	SEQ ID NO.
H53A (+23+47)	CTGAAGGTGTTCTTGTACTTCATCC	609
h53AON1	CTGTTGCCTCCGGTTCTG	610
H53A (-12+10)	ATTCTTTCAACTAGAATAAAAG	611
huEx45.30.66	GCCATCCTGGAGTTCTGTAAAGATACC AAA	612
HuEx45.30.71	CCAATGCCATCCTGGAGTTCTGTAAAG ATA	613
huEx45.30.79	GCCGCTGCCAATGCCATCCTGGAGTT CCT	614
huEx45.30.83	GTTTGCCGCTGCCAATGCCATCCTGG AGT	615
huEx45.30.88	CAACAGTTGCCGCTGCCAATGCCAT CCT	616
huEx45.30.92	CTGACAAACAGTTGCCGCTGCCAATG CCA	617
huEx45.30.96	TGTTCTGACAACAGTTGCCGCTGCC AAT	618
huEx45.30.99	CAATGTTCTGACAACAGTTGCCGCTG CCC	619
huEx45.30.103	CATTCAATGTTCTGACAACAGTTGCCG CT	620
huEx45.30.120	TATTTCTTCCCCAGTTGCATTCAATGTT CT	621
huEx45.30.127	GCTGAATTATTTCTTCCCCAGTTGCATT CA	622
huEx45.30.132	GGATTGCTGAATTATTTCTTCCCCAGTT GC	623
huEx45.30.137	TTTGAGGATTGCTGAATTATTTCTTCCC CA	624
huEx53.30.84	GTACTTCATCCCACTGATTCTGAATTCT TT	625
huEx53.30.88	TCTTGTACTTCATCCCACTGATTCTGAA TT	626
huEx53.30.91	TGTTCTTGTACTTCATCCCACTGATTCT GA	627
huEx53.30.103	CGGTTCTGAAGGTGTTCTGTACTTCAT CC	628
huEx53.30.106	CTCCGGTTCTGAAGGTGTTCTGTACTT CA	629
huEx53.30.109	TGCCTCCGGTTCTGAAGGTGTTCTGTAA CT	630
huEx53.30.112	TGTTGCCTCCGGTTCTGAAGGTGTTCTT GT	631
huEx53.30.115	AACTGTTGCCTCCGGTTCTGAAGGTGT TCT	632

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Name	Sequences	SEQ ID NO.
huEx53.30.118	TTCAACTGTTGCCTCCGGTTCTGAAGGT GT	633
h50AON1		
h50AON2		
	<u>Peptide Transporters (NH₂ to COOH) *:</u>	
rTAT	RRRQRRKKRC	570
R ₉ F ₂	RRRRRRRRRFFC	571
(RRAhx) ₄ B	RRAhxRRAhxRRAhxRRAhxB	572
(RAhxR) ₄ AhxB; (P007)	RAhxRRAhxRRAhxRRAhxRRAhxB	573
(AhxRR) ₄ AhxB	AhxRRAhxRRAhxRRAhxRRAhxB	574
(RAhx) ₆ B	RAhxRAhxRAhxRAhxRAhxRAhxB	575
(RAhx) ₈ B	RAhxRAhxRAhxRAhxRAhxRAhxRAhxB	576
(RAhxR) ₅ AhxB	RAhxRRAhxRRAhxRRAhxRRAhxB	577
(RAhxRRBR) ₂ AhxB; (CPO6062)	RAhxRRBRRAhxRRBRAhxB	578
MSP	ASSLNIA	579
	<u>Cell Penetrating Peptide/Homing Peptide/PMO Conjugates (NH₂ to COOH and 5' to 3')</u>	
MSP-PMO	ASSLNIA-XB- GCCAAACCTCGGTTACCTGAAAT	580 636
CP06062-MSP-PMO	RXRRBRRXRRBR-XB-ASSLNIA-X- GCCAAACCTCGGTTACCTGAAAT	581 636
MSP-CP06062-PMO	ASSLNIA-X-RXRRBRRXRRBR-B- GCCAAACCTCGGTTACCTGAAAT	582 636
CP06062-PMO	RXRRBRRXRRBR-XB- GCCAAACCTCGGTTACCTGAAAT	583 636

*Ahx is 6-aminoheptanoic acid and B is beta-alanine.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 651

<210> SEQ ID NO 1

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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ctgcaggtaa aagcatatgg atcaa

25

<210> SEQ ID NO 2

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<400> SEQUENCE: 2

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25

<210> SEQ ID NO 3
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<220> FEATURE:
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<400> SEQUENCE: 3

gtcaaatatcgc ctgcaggtaa aagca

25

<210> SEQ ID NO 4
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 4

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25

<210> SEQ ID NO 5
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 5

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25

<210> SEQ ID NO 6
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<212> TYPE: DNA
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<400> SEQUENCE: 6

tttctcaaca gatctgtcaa atcgc

25

<210> SEQ ID NO 7
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 7

ccatttctca acagatctgt caaat

25

<210> SEQ ID NO 8
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 8

ataatgaaaa cggccgcatt tctca

25

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aaatatctt atatcataat gaaaa

25

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<400> SEQUENCE: 10

tgttagccac tgattaaata tcttt

25

<210> SEQ ID NO 11
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<400> SEQUENCE: 11

aaactgttca gcttctgtta gccac

25

<210> SEQ ID NO 12
<211> LENGTH: 25
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 12

tttgttcttt ctgagaaaact gttca

25

<210> SEQ ID NO 13
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 13

ccaattctca ggaatttg tg tcttt

25

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<210> SEQ ID NO 14
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<212> TYPE: DNA
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<400> SEQUENCE: 14

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25

<210> SEQ ID NO 15
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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proprocessed human dystrophin

<400> SEQUENCE: 15

cttaagatac catttgtatt tagca

25

<210> SEQ ID NO 16
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 16

cTTacacctaa gataccattt gtatt

25

<210> SEQ ID NO 17
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 17

aaagacttac cttaagatac cattt

25

<210> SEQ ID NO 18
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 18

aaatcaaaga cttacacctaa gatac

25

<210> SEQ ID NO 19
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 19

aaaacaatc aaagacttac cttaa

25

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<210> SEQ ID NO 20
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 20

tcgaaaaaac aaatcaaaga cttac 25

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<210> SEQ ID NO 21
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 21

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<210> SEQ ID NO 22
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 22

cctgttaagat accaaaaagg caaaa 25

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<210> SEQ ID NO 23
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 23

agttccctgta agataccaa aaggc 25

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<210> SEQ ID NO 24
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 24

gagttccctgt aagataccaa aaagg 25

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<210> SEQ ID NO 25
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 25

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cctggagttc ctgtaagata ccaaa 25

<210> SEQ ID NO 26
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 26

tcctggagtt cctgtaaat accaa 25

<210> SEQ ID NO 27
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 27

gccatccctgg agttcctgtt agata 25

<210> SEQ ID NO 28
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 28

tgcacatccctg gagttcctgtt aagat 25

<210> SEQ ID NO 29
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 29

ccaatgccat cctggagttc ctgtt 25

<210> SEQ ID NO 30
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 30

cccaatgcca tcctggagtt cctgtt 25

<210> SEQ ID NO 31
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 31
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<210> SEQ ID NO 32
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 32
cgctgccccaa tgcacatccctg gagtt                                25

<210> SEQ ID NO 33
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 33
aacagtttgc cgctgccccaa tgccca                                25

<210> SEQ ID NO 34
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 34
ctgacaacag tttgccgtg cccaa                                25

<210> SEQ ID NO 35
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 35
gttgcattca atgttctgac aacag                                25

<210> SEQ ID NO 36
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 36
gctgaattat ttcttccca gttgc                                25

<210> SEQ ID NO 37
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 37

attatttcctt ccccaagttgc attca

25

<210> SEQ ID NO 38

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 38

ggcatctgttt tttgaggatt gctga

25

<210> SEQ ID NO 39

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 39

tttgaggatt gctgaattat ttctt

25

<210> SEQ ID NO 40

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 40

aatttttcctt gtagaatact ggcatt

25

<210> SEQ ID NO 41

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 41

atactggcat ctgttttga ggatt

25

<210> SEQ ID NO 42

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 42

accgcagatt caggcttccc aattt

25

<210> SEQ ID NO 43

<211> LENGTH: 25

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 43

aattttcctt gtagaatact ggcatt 25

<210> SEQ ID NO 44
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 44

ctgtttgcag acctccctgcc accgc 25

<210> SEQ ID NO 45
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 45

agattcaggc ttccccatTT ttcct 25

<210> SEQ ID NO 46
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 46

ctcttttttc tgtctgacag ctgtt 25

<210> SEQ ID NO 47
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 47

acccctccctgcc acccgagatt caggc 25

<210> SEQ ID NO 48
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 48

cctacacctt ttttctgtct gacag 25

<210> SEQ ID NO 49

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 49

gacagctgtt tgcagaccc ctgcc 25

<210> SEQ ID NO 50
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 50

gtcgccctac ctctttttc tgtct 25

<210> SEQ ID NO 51
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 51

gatctgtcgc cctacctttt ttttc 25

<210> SEQ ID NO 52
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 52

tattagatct gtcgccccctac ctctt 25

<210> SEQ ID NO 53
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 53

attcctatta gatctgtcgc cctac 25

<210> SEQ ID NO 54
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 54

agataccaaa aaggccaaac 20

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<210> SEQ ID NO 55
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 55

aagataccaa aaaggcaaaa

20

<210> SEQ ID NO 56
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 56

cctgtaagat accaaaaagg

20

<210> SEQ ID NO 57
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 57

gagttcctgt aagataccaa

20

<210> SEQ ID NO 58
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 58

tcctggagtt cctgtaagat

20

<210> SEQ ID NO 59
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 59

tgcacatcctg gagttcctgt

20

<210> SEQ ID NO 60
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 60

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cccaatgcca tcctggagtt 20

<210> SEQ ID NO 61
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 61

cgctgcccaa tgccatcctg 20

<210> SEQ ID NO 62
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 62

ctgacaacag tttgccgtg 20

<210> SEQ ID NO 63
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 63

gttgcattca atgttctgac 20

<210> SEQ ID NO 64
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 64

attatttcctt ccccagttgc 20

<210> SEQ ID NO 65
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 65

tttgaggatt gctgaattat 20

<210> SEQ ID NO 66
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 66

atactggcat ctgttttga

20

<210> SEQ ID NO 67

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 67

aattttcctt gtagaatact

20

<210> SEQ ID NO 68

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 68

agattcaggc ttcccaattt

20

<210> SEQ ID NO 69

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 69

accttcctgcc accgcagatt

20

<210> SEQ ID NO 70

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 70

gacagctgtt tgcagacactc

20

<210> SEQ ID NO 71

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 71

ctcttttttc tgtctgacag

20

<210> SEQ ID NO 72

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of

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<400> SEQUENCE: 72
cctacacctt ttttctgtct 20

<210> SEQ ID NO 73
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 73
gtcgccctac ctctttttc 20

<210> SEQ ID NO 74
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 74
gatctgtcgc cctacacctt 20

<210> SEQ ID NO 75
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 75
tattagatct gtcggccctac 20

<210> SEQ ID NO 76
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 76
attcctatta gatctgtcgc 20

<210> SEQ ID NO 77
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 77
gggggatttg agaaaataaa attac 25

<210> SEQ ID NO 78
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 78

atttgagaaa ataaaattac cttga

25

<210> SEQ ID NO 79
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 79

ctaggcctgga gaaagaagaa taaaa

25

<210> SEQ ID NO 80
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 80

agaaaataaaa attaccgttga cttgc

25

<210> SEQ ID NO 81
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 81

ttctttcttagc ctggagaaaag aagaa

25

<210> SEQ ID NO 82
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 82

ataaaaattac cttgacttgc tcaag

25

<210> SEQ ID NO 83
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 83

ttttgttctt ctagcctgga gaaag

25

<210> SEQ ID NO 84
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 84

attacaccttga cttgctcaag ctttt

25

<210> SEQ ID NO 85
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 85

tattcttttg ttcttcttagc ctggaa

25

<210> SEQ ID NO 86
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 86

cttgacttgc tcaagctttt ctttt

25

<210> SEQ ID NO 87
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 87

caagatattc ttttgttctt ctagc

25

<210> SEQ ID NO 88
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 88

cttttagtttg ctgtctttt ccagg

25

<210> SEQ ID NO 89
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 89

ccaggttcaa gtgggatact agcaa

25

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<210> SEQ ID NO 90
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 90

atctcttga aattctgaca agata 25

<210> SEQ ID NO 91
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 91

agcaatgtta tctgcttcct ccaac 25

<210> SEQ ID NO 92
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 92

aacaaattca tttaaatctc tttga 25

<210> SEQ ID NO 93
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 93

ccaaccataa aacaaattca tttaa 25

<210> SEQ ID NO 94
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 94

ttcctccaaac cataaaacaa attca 25

<210> SEQ ID NO 95
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 95

ttaaatctc tttgaaattc tgaca 25

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<210> SEQ ID NO 96
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 96

tgacaagata ttctttgtt cttct 25

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<210> SEQ ID NO 97
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 97

tcaaatggg atactagcaa tgtta 25

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<210> SEQ ID NO 98
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 98

agatattctt ttgttcttct agcct 25

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<210> SEQ ID NO 99
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 99

ctgtctttt ccagggttcaa gtggg 25

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<210> SEQ ID NO 100
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 100

ttctttgtt cttctagcct ggaga 25

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<210> SEQ ID NO 101
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 101

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cttttctttt agttgctgct ctttt	25
<210> SEQ ID NO 102	
<211> LENGTH: 25	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin	
<400> SEQUENCE: 102	
ttgttcttct agcctggaga aagaa	25
<210> SEQ ID NO 103	
<211> LENGTH: 25	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin	
<400> SEQUENCE: 103	
cttcttagcct ggagaaaagaa gaata	25
<210> SEQ ID NO 104	
<211> LENGTH: 25	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin	
<400> SEQUENCE: 104	
agcctggaga aagaagaata aaatt	25
<210> SEQ ID NO 105	
<211> LENGTH: 25	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin	
<400> SEQUENCE: 105	
ctggagaaaag aagaataaaa ttgtt	25
<210> SEQ ID NO 106	
<211> LENGTH: 20	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin	
<400> SEQUENCE: 106	
gaaagaagaa taaaattgtt	20
<210> SEQ ID NO 107	
<211> LENGTH: 20	
<212> TYPE: DNA	
<213> ORGANISM: Artificial Sequence	
<220> FEATURE:	
<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin	

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<400> SEQUENCE: 107

ggagaaaagaa gaataaaattt

20

<210> SEQ ID NO 108

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 108

agcctggaga aagaagaata

20

<210> SEQ ID NO 109

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 109

cttcttagcct ggagaaaagaa

20

<210> SEQ ID NO 110

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 110

tgtttttttt agcctggaga

20

<210> SEQ ID NO 111

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 111

ttttttttttt cttcttagcct

20

<210> SEQ ID NO 112

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 112

tgacaagata ttttttttttt

20

<210> SEQ ID NO 113

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 113

atctcttga aattctgaca

20

<210> SEQ ID NO 114

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 114

aacaaattca tttaaatctc

20

<210> SEQ ID NO 115

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 115

ttcctccaaac cataaaacaa

20

<210> SEQ ID NO 116

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 116

agcaatgtta tctgcttcct

20

<210> SEQ ID NO 117

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 117

tcaagtggg atactagcaa

20

<210> SEQ ID NO 118

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 118

ctgctctttt ccaggttcaa

20

<210> SEQ ID NO 119

<211> LENGTH: 20

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 119

cttttctttt agttgctgct

20

<210> SEQ ID NO 120
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 120

cttgacttg c tcaagcttt

20

<210> SEQ ID NO 121
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 121

attaccttga cttgctcaag

20

<210> SEQ ID NO 122
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 122

ataaaaattac cttgacttg

20

<210> SEQ ID NO 123
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 123

agaaaaataaa attaccttga

20

<210> SEQ ID NO 124
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 124

atttgagaaaa ataaaattac

20

<210> SEQ ID NO 125

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 125

gggggatttg agaaaataaa 20

<210> SEQ ID NO 126
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 126

ctgaaacaga caaatgcAAC aacgt 25

<210> SEQ ID NO 127
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 127

agtaactgaa acagacaaat gcaac 25

<210> SEQ ID NO 128
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 128

ccaccaggtaa ctgaaacaga caaat 25

<210> SEQ ID NO 129
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 129

ctcttccacc agtaactgaa acaga 25

<210> SEQ ID NO 130
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 130

ggcaactctt ccaccaggtaa ctgaa 25

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<210> SEQ ID NO 131
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 131

gcaggggcaaa ctcttccacc agtaa

25

<210> SEQ ID NO 132
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 132

ctggcgcagg ggcaactttt ccacc

25

<210> SEQ ID NO 133
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 133

ttaattgtt tgagaattcc ctggc

25

<210> SEQ ID NO 134
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 134

ttgtttgaga attccctggc gcagg

25

<210> SEQ ID NO 135
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 135

gcacggtcc tccagttca tttaa

25

<210> SEQ ID NO 136
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 136

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tccagttca ttaattgtt tgaga 25

<210> SEQ ID NO 137
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 137

gcttatggga gcacttacaa gcacg 25

<210> SEQ ID NO 138
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 138

tacaaggcacg ggtcctccag tttca 25

<210> SEQ ID NO 139
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 139

agtttatctt gctttctgg gctta 25

<210> SEQ ID NO 140
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 140

tctgctttag cttatttca agttt 25

<210> SEQ ID NO 141
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 141

atcttgctct tctgggctta tggga 25

<210> SEQ ID NO 142
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 142
ctttatccac tggagatttg tctgc                                25

<210> SEQ ID NO 143
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 143
cttattttca agtttatctt gctct                                25

<210> SEQ ID NO 144
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 144
ctaaccttta tccactggag atttg                                25

<210> SEQ ID NO 145
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 145
atttgtctgc ttgagcttat ttca                                25

<210> SEQ ID NO 146
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 146
aatgtctaac ctttatccac tggag                                25

<210> SEQ ID NO 147
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 147
tggtaatgt ctaaccttta tccac                                25

<210> SEQ ID NO 148
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 148

agagatggtt aatgtctaac ctta

25

<210> SEQ ID NO 149

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 149

acggaagaga tggtaatgt ctaac

25

<210> SEQ ID NO 150

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 150

acagacaat gcaacaacgt

20

<210> SEQ ID NO 151

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 151

ctgaaacaga caaatgcaac

20

<210> SEQ ID NO 152

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 152

agtaactgaa acagacaat

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<210> SEQ ID NO 153

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 153

ccaccagtaa ctgaaacaga

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<210> SEQ ID NO 154

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 154

ctcttccacc agtaactgaa

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<210> SEQ ID NO 155
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 155

ggcaactttt ccaccagtaa

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<210> SEQ ID NO 156
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 156

ctggcgcgagg ggcaactttt

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<210> SEQ ID NO 157
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 157

ttgtttgaga attccctggc

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<210> SEQ ID NO 158
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 158

tccagtttca tttaattgtt

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<210> SEQ ID NO 159
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 159

tacaaggcacg ggtcctccag

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<210> SEQ ID NO 160
<211> LENGTH: 20

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 160

gcttatggga gcacttacaa

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<210> SEQ ID NO 161
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 161

atcttgctct tctgggctta

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<210> SEQ ID NO 162
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 162

catttttca agtttatctt

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<210> SEQ ID NO 163
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 163

atttgtctgc ttgagcttat

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<210> SEQ ID NO 164
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 164

ctttatccac tggagatttg

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<210> SEQ ID NO 165
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 165

ctaaccttta tccactggag

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<210> SEQ ID NO 166
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 166

aatgtctaac ctttatccac

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<210> SEQ ID NO 167
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 167

tggtaatgt ctaaccctta

20

<210> SEQ ID NO 168
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 168

agagatgggtt aatgtctaac

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<210> SEQ ID NO 169
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 169

acggaagaga tggtaatgt

20

<210> SEQ ID NO 170
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 170

ctgaaaggaa aatacattt aaaaa

25

<210> SEQ ID NO 171
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 171

cctgaaaggaa aaatacattt taaaa

25

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<210> SEQ ID NO 172
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 172

gaaacacctgaa agggaaaatac atttt 25

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<210> SEQ ID NO 173
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 173

gaaaaacctga aaggaaaata cattt 25

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<210> SEQ ID NO 174
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 174

ctctggaaac ctgaaaggaa aatac 25

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<210> SEQ ID NO 175
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 175

gctctggaaa cctgaaaggaa aaata 25

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<210> SEQ ID NO 176
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 176

gttaaagctt gaaaaacctga aagga 25

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<210> SEQ ID NO 177
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 177

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tcaggtaaag ctctggaaac ctgaa	25
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ctcaggtaaa gctctggaaa cctga	25
 <pre><210> SEQ ID NO 179 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
 <pre><400> SEQUENCE: 179</pre>	
gtttctcagg taaagctctg gaaac	25
 <pre><210> SEQ ID NO 180 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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tgtttctcag gtaaagctct ggaaa	25
 <pre><210> SEQ ID NO 181 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
 <pre><400> SEQUENCE: 181</pre>	
aatttctcct tgtttctcag gtaaa	25
 <pre><210> SEQ ID NO 182 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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tttgagctc aatttctcct tgttt	25
 <pre><210> SEQ ID NO 183 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	

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<400> SEQUENCE: 183
ttttatgttga gcttcaattt ctcct 25

<210> SEQ ID NO 184
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 184
aagctgcccc aaggctttta tttga 25

<210> SEQ ID NO 185
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 185
aggccttcaa gcttttttc aagct 25

<210> SEQ ID NO 186
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 186
ttcaagctt ttttcaagct gccca 25

<210> SEQ ID NO 187
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 187
gatgatttaa ctgccttca aggtc 25

<210> SEQ ID NO 188
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 188
ctgccttca aggtcttcaa gcttt 25

<210> SEQ ID NO 189
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 189

aggagataac cacagcagca gatga

25

<210> SEQ ID NO 190

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 190

cagcagatga tttaactgct cttca

25

<210> SEQ ID NO 191

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 191

atttccaact gattcctaat aggag

25

<210> SEQ ID NO 192

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 192

cttggtttgg ttgggtataa atttc

25

<210> SEQ ID NO 193

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 193

caactgattc ctaataggag ataac

25

<210> SEQ ID NO 194

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 194

cttaacgtca aatggtcctt cttgg

25

<210> SEQ ID NO 195

<211> LENGTH: 25

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 195

ttggttataa atttccaaact gattc

25

<210> SEQ ID NO 196
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 196

ccttacacctt aa cgtcaatgg tcctt

25

<210> SEQ ID NO 197
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 197

tccttcttgg tttgggttgttataa

25

<210> SEQ ID NO 198
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 198

agttccctac cttaaacgtca aatgg

25

<210> SEQ ID NO 199
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 199

caaaaagttc cctacacctt aa cgtca

25

<210> SEQ ID NO 200
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 200

ttaaaggaaaa agttccctac cttaa

25

<210> SEQ ID NO 201

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 201

atatttaaag caaaaagtc cctac

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<210> SEQ ID NO 202
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 202

aggaaaatac attttaaaaa

20

<210> SEQ ID NO 203
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 203

aaggaaaata cattttaaaa

20

<210> SEQ ID NO 204
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 204

cctgaaagga aaatacattt

20

<210> SEQ ID NO 205
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 205

ggaaacctga aaggaaaata

20

<210> SEQ ID NO 206
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 206

gctctggaaa cctgaaagga

20

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<210> SEQ ID NO 207
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 207

gtaaaagctct ggaaacacctga

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<210> SEQ ID NO 208
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 208

ctcaggtaaa gctctggaaa

20

<210> SEQ ID NO 209
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 209

aatttctcct tgtttctcag

20

<210> SEQ ID NO 210
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 210

ttttatttga gcttcaattt

20

<210> SEQ ID NO 211
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 211

aagctgcccc aggtctttta

20

<210> SEQ ID NO 212
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 212

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ttaaaggcttt ttttcaagct 20

<210> SEQ ID NO 213
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 213

ctgctcttca aggtcttcaa 20

<210> SEQ ID NO 214
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 214

cagcagatga tttaactgct 20

<210> SEQ ID NO 215
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 215

aggagataac cacagcagca 20

<210> SEQ ID NO 216
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 216

caactgatttc ctaataggag 20

<210> SEQ ID NO 217
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 217

ttggttataaa atttccaaact 20

<210> SEQ ID NO 218
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 218
tccttcttgg tttgggttgt 20

<210> SEQ ID NO 219
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 219
cttaacgtca aatggtcatt 20

<210> SEQ ID NO 220
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 220
cctacacctaa cgtcaaatgg 20

<210> SEQ ID NO 221
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 221
agttccctac cttaacgtca 20

<210> SEQ ID NO 222
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 222
caaaaagtgc cctacacctaa 20

<210> SEQ ID NO 223
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 223
taaagcaaaa agttccctac 20

<210> SEQ ID NO 224
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of

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<400> SEQUENCE: 224

atatttaaag caaaaagttc

20

<210> SEQ ID NO 225

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 225

ctggggaaaa gaacccatat agtgc

25

<210> SEQ ID NO 226

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 226

tcctgggaa aagaacccat atagt

25

<210> SEQ ID NO 227

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 227

gtttcctggg gaaaagaacc catat

25

<210> SEQ ID NO 228

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 228

cagtttcctg gggaaaagaa cccat

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<210> SEQ ID NO 229

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin

<400> SEQUENCE: 229

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<210> SEQ ID NO 230

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 230

tatttcagtt tcctggggaa aagaa

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<210> SEQ ID NO 231
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 231

tgctatttca gtttcctggg gaaaa

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<210> SEQ ID NO 232
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 232

actgctattt cagtttcctg gggaa

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<210> SEQ ID NO 233
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 233

tgaactgcta tttcagtttc ctggg

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<210> SEQ ID NO 234
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 234

cttgaactgc tatttcagtt tcctg

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<210> SEQ ID NO 235
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 235

tagcttgaac tgctatttca gtttc

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<210> SEQ ID NO 236
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 236

ttagcttga actgcttattt cagtt

25

<210> SEQ ID NO 237
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 237

ttccacatcc ggttgttag cttaga

25

<210> SEQ ID NO 238
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 238

tgcccttag acaaaatctc ttcca

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<210> SEQ ID NO 239
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 239

ttagacaaa atctcttcca catcc

25

<210> SEQ ID NO 240
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 240

gttttcctt gtacaaaatgc tgccc

25

<210> SEQ ID NO 241
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 241

gtacaaaatgc tgcccttag acaaa

25

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<210> SEQ ID NO 242
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 242

cttcactggc tgagtggtcg gttt 25

<210> SEQ ID NO 243
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 243

ggctgggttt tccttgtaca aatgc 25

<210> SEQ ID NO 244
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 244

attacacctca ctggctgagt ggctg 25

<210> SEQ ID NO 245
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 245

gcttcattac cttcactggc tgagt 25

<210> SEQ ID NO 246
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 246

aggttgcttc attacacctca ctggc 25

<210> SEQ ID NO 247
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 247

gcttagagggtt gcttcattac cttca 25

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<210> SEQ ID NO 248
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 248

atattgctag aggttgcttc attac 25

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<210> SEQ ID NO 249
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 249

gaaaagaacc catatagtgc 20

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<210> SEQ ID NO 250
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 250

ggaaaaagaa cccatatagt 20

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<210> SEQ ID NO 251
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 251

tcctggggaa aagaacctat 20

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<210> SEQ ID NO 252
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 252

cagtttcctg gggaaaagaa 20

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<210> SEQ ID NO 253
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 253

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tat ttcagtt tcctggggaa 20

<210> SEQ ID NO 254
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 254

actgctattt cagtttcctg 20

<210> SEQ ID NO 255
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 255

cttgaactgc tat ttcagtt 20

<210> SEQ ID NO 256
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 256

ttagcttga actgctattt 20

<210> SEQ ID NO 257
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 257

ttccacatcc ggttgttag 20

<210> SEQ ID NO 258
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 258

ttagacaaa atctcttcca 20

<210> SEQ ID NO 259
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 259

gtacaaaatgc tgcccttttag

20

<210> SEQ ID NO 260

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 260

ggctgggttt tccttgtaca

20

<210> SEQ ID NO 261

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 261

cttcactggc tgagtggctg

20

<210> SEQ ID NO 262

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 262

attacacctca ctggctgagt

20

<210> SEQ ID NO 263

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 263

gcttcattac cttcactggc

20

<210> SEQ ID NO 264

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 264

aggttgcttc attacacctca

20

<210> SEQ ID NO 265

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 265

gctagagggtt gcttcattac

20

<210> SEQ ID NO 266

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 266

atattgcttag aggttgcttc

20

<210> SEQ ID NO 267

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 267

ctttaacaga aaagcataca catta

25

<210> SEQ ID NO 268

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 268

tcctctttaa cagaaaagca tacac

25

<210> SEQ ID NO 269

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 269

tccctcttta acagaaaagc ataca

25

<210> SEQ ID NO 270

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 270

taacttcctc tttaacagaa aagca

25

<210> SEQ ID NO 271

<211> LENGTH: 25

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 271

ctaacatccct ctttaacaga aaagc

25

<210> SEQ ID NO 272
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 272

tcttcttaact tcctctttaa cagaa

25

<210> SEQ ID NO 273
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 273

atcttcttaac ttccctttta acaga

25

<210> SEQ ID NO 274
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 274

tcagatcttc taacttcctc tttaa

25

<210> SEQ ID NO 275
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 275

ctcagatctt ctaacttcct ctta

25

<210> SEQ ID NO 276
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 276

agagctcaga tcttcttaact tcctc

25

<210> SEQ ID NO 277

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 277

cagagctcag atcttctaac ttccct

25

<210> SEQ ID NO 278
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 278

cactcagagc tcagatcttc tact

24

<210> SEQ ID NO 279
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 279

ccttccactc agagctcaga tcttc

25

<210> SEQ ID NO 280
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 280

gttaaacgggtt taccgccttc cactc

25

<210> SEQ ID NO 281
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 281

ctttgccctc agctcttgaa gtaaa

25

<210> SEQ ID NO 282
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 282

ccctcagctc ttgaagtaaa cggtt

25

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<210> SEQ ID NO 283
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 283

ccaggagcta ggtcaggctg ctttg

25

<210> SEQ ID NO 284
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 284

ggtcaggctg cttgccctc agctc

25

<210> SEQ ID NO 285
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 285

aggctccaat agtggtcagt ccagg

25

<210> SEQ ID NO 286
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 286

tcagtccagg agcttaggtca ggctg

25

<210> SEQ ID NO 287
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 287

cttacaggtt ccaatagtgg tcagt

25

<210> SEQ ID NO 288
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 288

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gtatacttac aggctcaat agtgg	25
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atccagtata cttacaggct ccaat	25
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atgggatcca gtatacttac aggct	25
 <pre><210> SEQ ID NO 291 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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agagaatggg atccagtata cttac	25
 <pre><210> SEQ ID NO 292 <211> LENGTH: 20 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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acagaaaaagc atacacattaa	20
 <pre><210> SEQ ID NO 293 <211> LENGTH: 20 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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ttaaacagaa aagcatacac	20
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<400> SEQUENCE: 294

tcctttaaa cagaaaagca

20

<210> SEQ ID NO 295

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 295

taacttcctc tttaacagaa

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<210> SEQ ID NO 296

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 296

tcttctaact tcctttaaa

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<210> SEQ ID NO 297

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 297

tcagatcttc taacttcctc

20

<210> SEQ ID NO 298

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 298

cttccactc agagctcaga

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<210> SEQ ID NO 299

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 299

gttaaacggtt taccgccttc

20

<210> SEQ ID NO 300

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of

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<400> SEQUENCE: 300
ccctcagctc ttgaagtaaa 20

<210> SEQ ID NO 301
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 301
ggtcaggctg ctttgccctc 20

<210> SEQ ID NO 302
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 302
tcagtccagg agcttaggtca 20

<210> SEQ ID NO 303
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 303
aggctccaat agtggtcagt 20

<210> SEQ ID NO 304
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 304
cttacaggct ccaatagtg 20

<210> SEQ ID NO 305
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 305
gtatacttac aggctccaat 20

<210> SEQ ID NO 306
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 306

atccagta cttacaggct

20

<210> SEQ ID NO 307
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 307

atgggatcca gtatacttac

20

<210> SEQ ID NO 308
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 308

agagaatggg atccagta

20

<210> SEQ ID NO 309
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 309

ctaaaatatt ttgggtttt gcaaaa

26

<210> SEQ ID NO 310
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 310

gctaaaatat ttgggtttt tgcaaa

26

<210> SEQ ID NO 311
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 311

taggagctaa aatattttgg gttttt

26

<210> SEQ ID NO 312
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 312

agttaggagct aaaatatttt gggtt

25

<210> SEQ ID NO 313
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 313

tgagtaggag ctaaaatatt ttggg

25

<210> SEQ ID NO 314
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 314

ctgagtagga gctaaaatat tttggg

26

<210> SEQ ID NO 315
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 315

cagtctgagt aggagctaaa atatt

25

<210> SEQ ID NO 316
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 316

acagtctgag taggagctaa aatatt

26

<210> SEQ ID NO 317
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 317

gagtaacagt ctgagtagga gctaaa

26

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<210> SEQ ID NO 318
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 318

cagagtaaca gtctgagtag gagct

25

<210> SEQ ID NO 319
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 319

caccagagta acagtctgag taggag

26

<210> SEQ ID NO 320
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 320

gtcaccagag taacagtctg agtag

25

<210> SEQ ID NO 321
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 321

aaccacaggt tgtgtcacca gagtaa

26

<210> SEQ ID NO 322
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 322

tttgtgtcac cagagtaaca gtctg

25

<210> SEQ ID NO 323
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 323

tggcagtttc cttagtaacc acaggt

26

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<210> SEQ ID NO 324
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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```
<400> SEQUENCE: 324
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```
atttctagtt tggagatggc agtttc 26
```

```
<210> SEQ ID NO 325
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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```
<400> SEQUENCE: 325
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```
ggaagatggc atttctagtt tggag 25
```

```
<210> SEQ ID NO 326
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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```
<400> SEQUENCE: 326
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```
catcaaggaa gatggcattt cttagtt 26
```

```
<210> SEQ ID NO 327
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

```
<400> SEQUENCE: 327
```

```
gagcaggtac ctccaacatc aaggaa 26
```

```
<210> SEQ ID NO 328
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

```
<400> SEQUENCE: 328
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```
atctgccaga gcaggtacct ccaac 25
```

```
<210> SEQ ID NO 329
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 329
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aagttctgtc caagcccggt tgaat 26

<210> SEQ ID NO 330
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 330

cggttgaaat ctgccagac aggtac 26

<210> SEQ ID NO 331
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 331

gagaaggcca gtcggtaagt tctgtc 26

<210> SEQ ID NO 332
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 332

gtcggtaagt tctgtccaag cccgg 25

<210> SEQ ID NO 333
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 333

ataaacttgat caagcagaga aagcca 26

<210> SEQ ID NO 334
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 334

aagcagagaa agccagtcgg taagt 25

<210> SEQ ID NO 335
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 335
caccctctgt gatTTATAA ctTgat                                26

<210> SEQ ID NO 336
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 336
caaggtaacc caccatcacc ctctgt                                26

<210> SEQ ID NO 337
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 337
catcacccTC tGTGATTtTA taact                                25

<210> SEQ ID NO 338
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 338
cttctgcttg atgatcatct cgTTGA                                26

<210> SEQ ID NO 339
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 339
cTTCTGCTT gATGATCATC TCGTTG                                26

<210> SEQ ID NO 340
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 340
atctcgTTGA tATCCTCAAG gTCACC                                26

<210> SEQ ID NO 341
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 341

tcataaccttc tgcttgatga tcatct

26

<210> SEQ ID NO 342

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 342

tcatttttcc tcataaccttc tgcttg

26

<210> SEQ ID NO 343

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 343

ttttctcata ccttctgttt gatgtat

26

<210> SEQ ID NO 344

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 344

ttttatcatt ttttctcata ccttct

26

<210> SEQ ID NO 345

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 345

ccaactttta tcatttttc tcatac

26

<210> SEQ ID NO 346

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 346

atattttggg ttttgcaaa

20

<210> SEQ ID NO 347

<211> LENGTH: 20

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 347

aaaatatttt gggttttgc

20

<210> SEQ ID NO 348
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 348

gagctaaaaat attttgggtt

20

<210> SEQ ID NO 349
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 349

agttaggagct aaaatatttt

20

<210> SEQ ID NO 350
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 350

gtctgagtag gagctaaaaat

20

<210> SEQ ID NO 351
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 351

taacagtctg agttaggagct

20

<210> SEQ ID NO 352
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 352

cagagtaaca gtctgagtag

20

<210> SEQ ID NO 353

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 353

cacaggttgt gtcaccagag

20

<210> SEQ ID NO 354
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 354

agtttcctta gtaaccacag

20

<210> SEQ ID NO 355
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 355

tagtttgag atggcagttt

20

<210> SEQ ID NO 356
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 356

ggaagatggc atttcttagtt

20

<210> SEQ ID NO 357
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 357

tacctccaac atcaaggaag

20

<210> SEQ ID NO 358
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 358

atctgccaga gcaggtacct

20

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<210> SEQ ID NO 359
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 359

ccaagcccggttgaaatctg

20

<210> SEQ ID NO 360
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 360

gtcggtaagt tctgtccaag

20

<210> SEQ ID NO 361
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 361

aagcagagaa agccagtcgg

20

<210> SEQ ID NO 362
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 362

tttataact tgatcaagca

20

<210> SEQ ID NO 363
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 363

catcacccctctgtgatttta

20

<210> SEQ ID NO 364
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 364

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ctcaaggta cccaccatca 20

<210> SEQ ID NO 365
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 365

catctcgttg atatcctcaa 20

<210> SEQ ID NO 366
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 366

cttctgcttg atgatcatct 20

<210> SEQ ID NO 367
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 367

cataccttct gcttgatgat 20

<210> SEQ ID NO 368
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 368

tttctcatac cttctgcttg 20

<210> SEQ ID NO 369
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 369

catttttctt cataccttct 20

<210> SEQ ID NO 370
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 370
tttacattt tttctcatac 20

<210> SEQ ID NO 371
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 371
caacttttat catttttct 20

<210> SEQ ID NO 372
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 372
ctgttaagaac aaatatccct tagta 25

<210> SEQ ID NO 373
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 373
tgcctgtaaag aacaatatac cctta 25

<210> SEQ ID NO 374
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 374
gttgccctgta agaacaaaata tccct 25

<210> SEQ ID NO 375
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 375
atgttgtgcct gtaagaacaa atatac 25

<210> SEQ ID NO 376
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 376

gcattgtgc ctgtaagaac aaata

25

<210> SEQ ID NO 377
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 377

cctgcattgt tgccctgaag aacaa

25

<210> SEQ ID NO 378
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 378

atcctgcatt gttccctgta agaac

25

<210> SEQ ID NO 379
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 379

caaattcctgc attgttgcct gtaag

25

<210> SEQ ID NO 380
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 380

tccaaatcct gcattgtgc ctgta

25

<210> SEQ ID NO 381
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 381

tgttccaaat cctgcattgt tgcct

25

<210> SEQ ID NO 382
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 382

tctgttccaa atcctgcatt gttgc

25

<210> SEQ ID NO 383
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 383

aactggggac gcctctgttc caaat

25

<210> SEQ ID NO 384
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 384

gcctctgttc caaatcctgc attgt

25

<210> SEQ ID NO 385
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 385

cagcgtaat gagttcttcc aactg

25

<210> SEQ ID NO 386
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 386

cttccaactg gggacgcctc tgttc

25

<210> SEQ ID NO 387
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 387

cttggttttc aaatttggg cagcg

25

<210> SEQ ID NO 388
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 388

ctagccttctt gattgctgggt cttgt

25

<210> SEQ ID NO 389
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 389

ttttcaaatt ttggggcagcg gtaat

25

<210> SEQ ID NO 390
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 390

ttcgatccgt aatgattgtt cttagc

25

<210> SEQ ID NO 391
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 391

gattgctgggt ctgttttttc aaatt

25

<210> SEQ ID NO 392
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 392

cattacttcga tccgtaatga ttgtt

25

<210> SEQ ID NO 393
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 393

ttgttcttagc ctcttgattg ctgggt

25

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<210> SEQ ID NO 394
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 394

aaaaacttac ttcatccgt aatga

25

<210> SEQ ID NO 395
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 395

tgttaaaaaa cttacttcga tccgt

25

<210> SEQ ID NO 396
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 396

atgcttgta aaaaacttac ttca

25

<210> SEQ ID NO 397
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 397

gtccccatgtc tgttaaaaaa ctta

25

<210> SEQ ID NO 398
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 398

agaacaaata tccttagta

20

<210> SEQ ID NO 399
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 399

gtaagaacaa atatccctta

20

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<210> SEQ ID NO 400
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 400

tgcctgttaag aacaaatatac 20

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<210> SEQ ID NO 401
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 401

attgttgct tgaagaacaa 20

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<210> SEQ ID NO 402
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 402

cctgcattgt tgcctgttaag 20

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<210> SEQ ID NO 403
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 403

caaattcctgc attgttgctt 20

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<210> SEQ ID NO 404
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 404

gcctctgttc caaattcctgc 20

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<210> SEQ ID NO 405
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 405

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cttccaactg gggacgcctc 20

<210> SEQ ID NO 406
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 406

cagcggttaat gagttttcc 20

<210> SEQ ID NO 407
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 407

ttttcaaaatt ttggggcagcg 20

<210> SEQ ID NO 408
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 408

gattgctggc cttgttttc 20

<210> SEQ ID NO 409
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 409

ttgttcttagc ctcttgattg 20

<210> SEQ ID NO 410
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 410

ttcgatccgt aatgattgtt 20

<210> SEQ ID NO 411
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 411
cttacttcga tccgtaatga                                20

<210> SEQ ID NO 412
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 412
aaaaacttac ttcgatccgt                                20

<210> SEQ ID NO 413
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 413
tgttaaaaaa cttacttcga                                20

<210> SEQ ID NO 414
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 414
atgcttgta aaaaacttac                                20

<210> SEQ ID NO 415
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 415
gtccccatgct tgttaaaaaa                                20

<210> SEQ ID NO 416
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 416
ctagaataaaa agggaaaaata aatat                                25

<210> SEQ ID NO 417
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 417

aactagaata aaaggaaaaaa taaaat

25

<210> SEQ ID NO 418

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 418

ttcaactaga ataaaaggaa aaataa

25

<210> SEQ ID NO 419

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 419

cttcaacta gaataaaaagg aaaaaa

25

<210> SEQ ID NO 420

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 420

attctttcaa ctagaataaa aggaa

25

<210> SEQ ID NO 421

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 421

gaattcttc aactagaata aaagg

25

<210> SEQ ID NO 422

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 422

tctgaattct ttcaactaga ataaa

25

<210> SEQ ID NO 423

<211> LENGTH: 25

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 423

attctgaatt ctttcaacta gaata

25

<210> SEQ ID NO 424
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 424

ctgattctga attcttcaa ctaga

25

<210> SEQ ID NO 425
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 425

cactgattct gaattcttc aacta

25

<210> SEQ ID NO 426
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 426

tcccaactgat tctgaattct ttcaa

25

<210> SEQ ID NO 427
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 427

catcccactg attctgaatt ctttc

25

<210> SEQ ID NO 428
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 428

tacttcatcc cactgattct gaatt

25

<210> SEQ ID NO 429

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 429

ctgaagggtgt tcttgttactt catcc 25

<210> SEQ ID NO 430
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 430

cggttctgaa ggtgttcttg tact 24

<210> SEQ ID NO 431
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 431

ctgttgcctc cggttctgaa ggtgt 25

<210> SEQ ID NO 432
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 432

tttcattcaa ctgttgcctc cggtt 25

<210> SEQ ID NO 433
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 433

taacatttca ttcaactgtt gcctc 25

<210> SEQ ID NO 434
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 434

ttgtgttgaa tcctttaaca tttca 25

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<210> SEQ ID NO 435
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 435

tcttccttag cttccagcca ttgtg 25

<210> SEQ ID NO 436
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 436

ccttagcttcc agccatttg 25

<210> SEQ ID NO 437
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 437

gtcctaagac ctgctcagct tcttc 25

<210> SEQ ID NO 438
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 438

ctgctcagct tcttccttag cttcc 25

<210> SEQ ID NO 439
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 439

ctcaagttg gctctggct gtctt 25

<210> SEQ ID NO 440
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 440

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ggcctgtcct aagacctgct cagct	25
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tagggaccct cttccatga ctcaa	25
 <pre><210> SEQ ID NO 442 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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tttggattgc atctactgta taggg	25
 <pre><210> SEQ ID NO 443 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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accctcccttc catgactcaa gcttg	25
 <pre><210> SEQ ID NO 444 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
 <pre><400> SEQUENCE: 444</pre>	
cttgggtttct gtgattttct tttgg	25
 <pre><210> SEQ ID NO 445 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	
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atctactgta tagggaccct ctttc	25
 <pre><210> SEQ ID NO 446 <211> LENGTH: 25 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: Antisense sequence to target splice site of proprocessed human dystrophin</pre>	

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<400> SEQUENCE: 446

ctaacaccttgg tttctgtat tttct

25

<210> SEQ ID NO 447

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 447

tttcttttgg attgcatactaa ctgtat

25

<210> SEQ ID NO 448

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 448

tgataactaac cttgggttct gtgtat

25

<210> SEQ ID NO 449

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 449

atctttgata ctaaacaccttgg tttct

25

<210> SEQ ID NO 450

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 450

aaggatatctt tgataactaac cttgg

25

<210> SEQ ID NO 451

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 451

ttaaaaaggt atctttgata ctaaac

25

<210> SEQ ID NO 452

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of

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<400> SEQUENCE: 452

ataaaaaggaa aaataaaat

20

<210> SEQ ID NO 453
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 453

gaataaaaagg aaaaataaat

20

<210> SEQ ID NO 454
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 454

aactagaata aaaggaaaaa

20

<210> SEQ ID NO 455
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 455

ctttcaacta gaataaaaagg

20

<210> SEQ ID NO 456
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 456

gaattcttcaacta aactagaata

20

<210> SEQ ID NO 457
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 457

attctgaatt ctttcaacta

20

<210> SEQ ID NO 458
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 458

tacttcatcc cactgattct

20

<210> SEQ ID NO 459
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 459

ctgaaggtgt tcttgtact

19

<210> SEQ ID NO 460
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 460

ctgttgccctc cggttctgaa

20

<210> SEQ ID NO 461
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 461

taacatttca ttcaactgtt

20

<210> SEQ ID NO 462
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 462

ttgtgttgaa tcctttaaca

20

<210> SEQ ID NO 463
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 463

cttagcttcc agccattgtg

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<210> SEQ ID NO 464
<211> LENGTH: 20

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 464

ctgctcagct tcttccttag

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<210> SEQ ID NO 465
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 465

ggcctgtcct aagacctgct

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<210> SEQ ID NO 466
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 466

ctcaagcttg gctctggcct

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<210> SEQ ID NO 467
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 467

accctcccttc catgactcaa

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<210> SEQ ID NO 468
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 468

atctaactgta tagggaccct

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<210> SEQ ID NO 469
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 469

tttcttttgg attgcatacta

20

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<210> SEQ ID NO 470
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 470

cttggtttct gtgattttct 20

<210> SEQ ID NO 471
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 471

ctaacccttgg tttctgtat 20

<210> SEQ ID NO 472
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 472

tgataactaac ctgggtttct 20

<210> SEQ ID NO 473
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 473

atctttgata ctaacccttgg 20

<210> SEQ ID NO 474
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 474

aaggatatctt tgataactaac 20

<210> SEQ ID NO 475
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 475

ttaaaaaggt atctttgata 20

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<210> SEQ ID NO 476
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 476

ctatagattt ttatgagaaa gaga 24

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<210> SEQ ID NO 477
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 477

aactgctata gattttatg agaaaa 25

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<210> SEQ ID NO 478
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 478

tggccaaactg ctatagattt ttatg 25

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<210> SEQ ID NO 479
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 479

gtctttggcc aactgctata gattt 25

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<210> SEQ ID NO 480
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 480

cggagggtctt tggccaaactg ctata 25

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<210> SEQ ID NO 481
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
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<400> SEQUENCE: 481

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actggcgag gtcttggcc aactg 25

<210> SEQ ID NO 482
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 482

tttgtctgcc actggcgag gtctt 25

<210> SEQ ID NO 483
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 483

agtcatttgc cacatctaca tttgt 25

<210> SEQ ID NO 484
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 484

tttgccacat ctacatttgt ctgcc 25

<210> SEQ ID NO 485
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 485

cggagaagt ttcaaggcca agtca 25

<210> SEQ ID NO 486
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 486

gtatcatctg cagaataatc ccgga 25

<210> SEQ ID NO 487
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 487

taatcccgga gaagtttcag ggcca

25

<210> SEQ ID NO 488

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 488

ttagtcatgtg gactttctg gtatc

25

<210> SEQ ID NO 489

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 489

agaggcattt atattctctg ttatc

25

<210> SEQ ID NO 490

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 490

atgtggactt ttctggatc atctg

25

<210> SEQ ID NO 491

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 491

ctttttatgaa tgcttctcca agagg

25

<210> SEQ ID NO 492

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 492

atattctctg ttatcatgtg gactt

25

<210> SEQ ID NO 493

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 493

catacctttt atgaatgctt ctcca

25

<210> SEQ ID NO 494

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 494

ctccaagagg cattgatatt ctctg

25

<210> SEQ ID NO 495

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 495

taattcatac ctttatgaa tgott

25

<210> SEQ ID NO 496

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 496

cttttatgaa tgcttctcca agagg

25

<210> SEQ ID NO 497

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 497

taatgttaatt catacctttt atgaa

25

<210> SEQ ID NO 498

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 498

agaaaataatg taattcatac ctttt

25

<210> SEQ ID NO 499

<211> LENGTH: 25

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 499

gttttagaaa taatgtaatt catac

25

<210> SEQ ID NO 500
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 500

gattttatg agaaagaga

19

<210> SEQ ID NO 501
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 501

ctatagattt ttatgagaaa

20

<210> SEQ ID NO 502
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 502

aactgctata gattttatg

20

<210> SEQ ID NO 503
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 503

tggccaactg ctatagattt

20

<210> SEQ ID NO 504
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 504

gtctttggcc aactgctata

20

<210> SEQ ID NO 505

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 505

cggaggctt tggccaaactg 20

<210> SEQ ID NO 506
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 506

tttgtctgcc actggcgag 20

<210> SEQ ID NO 507
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 507

tttgccacat ctacatttgt 20

<210> SEQ ID NO 508
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 508

ttcagggcca agtcatttgc 20

<210> SEQ ID NO 509
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 509

taatcccgga gaagttcag 20

<210> SEQ ID NO 510
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 510

gtatcatctg cagaataatc 20

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<210> SEQ ID NO 511
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 511

atgtggactt ttctggatc

20

<210> SEQ ID NO 512
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 512

atattctctg ttatcatgtg

20

<210> SEQ ID NO 513
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 513

ctccaagagg cattgatatt

20

<210> SEQ ID NO 514
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 514

ctttatgaa tgcttctcca

20

<210> SEQ ID NO 515
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 515

cataccttt atgaatgttt

20

<210> SEQ ID NO 516
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 516

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taattcatac cttttatgaa 20

<210> SEQ ID NO 517
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 517

taatgtaatt cataccctttt 20

<210> SEQ ID NO 518
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 518

agaaataatg taattcatac 20

<210> SEQ ID NO 519
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 519

gttttagaaa taatgtaattt 20

<210> SEQ ID NO 520
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 520

ctgcaaagga ccaaatgttc agatg 25

<210> SEQ ID NO 521
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 521

tccccctgca aaggacaaaa tggttc 25

<210> SEQ ID NO 522
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 522
ctcactcacc ctgcaaagga ccaaa                                25

<210> SEQ ID NO 523
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 523
tctcgctcac tcaccctgca aagga                                25

<210> SEQ ID NO 524
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 524
cagcctctcg ctcactcacc ctgca                                25

<210> SEQ ID NO 525
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 525
caaaggcagcc tctcgctcac tcacc                                25

<210> SEQ ID NO 526
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 526
tcttccaaag cagcctctcg ctcac                                25

<210> SEQ ID NO 527
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 527
tctatgagtt tcttccaaag cagcc                                25

<210> SEQ ID NO 528
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 528
gttgcagtaa tctatgagg ttctc 25

<210> SEQ ID NO 529
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 529
gaactgttgc agtaatctat gagtt 25

<210> SEQ ID NO 530
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 530
ttccagggtcc agggggaaact gttgc 25

<210> SEQ ID NO 531
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 531
gtaagccagg caagaaaactt ttcca 25

<210> SEQ ID NO 532
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 532
ccaggcaaga aacttttcca ggtcc 25

<210> SEQ ID NO 533
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 533
tggcagttgt ttcagttct gtaag 25

<210> SEQ ID NO 534
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 534

ggtagcatcc tgttagacat tggca

25

<210> SEQ ID NO 535
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 535

gacattggca gttgtttcag cttct

25

<210> SEQ ID NO 536
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 536

tctaggagcc ttcccttacg ggtag

25

<210> SEQ ID NO 537
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 537

cttttactcc ctggagtc tctag

25

<210> SEQ ID NO 538
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 538

gagccttcc ttacggtag catcc

25

<210> SEQ ID NO 539
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 539

tgcatttgt ttcatcagct ctttt

25

<210> SEQ ID NO 540
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 540

cttggagtc tctaggagcc tttcc

25

<210> SEQ ID NO 541
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 541

cttacttgcc attgtttcat cagct

25

<210> SEQ ID NO 542
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 542

cagctctttt actcccttgg agtct

25

<210> SEQ ID NO 543
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 543

cctgacttac ttgccattgt ttcat

25

<210> SEQ ID NO 544
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 544

aaatgcctga cttacttgcc attgt

25

<210> SEQ ID NO 545
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 545

agcggaaatg cctgacttac ttgcc

25

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<210> SEQ ID NO 546
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 546

gctaaaggcg aaatgcctga cttac 25

<210> SEQ ID NO 547
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 547

aaggacaaa tgttcagatg 20

<210> SEQ ID NO 548
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 548

ctgcaaaggaa ccaaattgttc 20

<210> SEQ ID NO 549
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 549

tcaccctgca aaggacaaa 20

<210> SEQ ID NO 550
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 550

ctcaactcacc ctgcaaaggaa 20

<210> SEQ ID NO 551
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 551

tctcgctcac tcaccctgca 20

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```
<210> SEQ ID NO 552
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin
```

```
<400> SEQUENCE: 552
```

```
cagccctctcg ctcactcacc 20
```

```
<210> SEQ ID NO 553
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin
```

```
<400> SEQUENCE: 553
```

```
caaaggcagcc tctcgctaac 20
```

```
<210> SEQ ID NO 554
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin
```

```
<400> SEQUENCE: 554
```

```
tctatgagtt tcttccaaag 20
```

```
<210> SEQ ID NO 555
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin
```

```
<400> SEQUENCE: 555
```

```
gaactgttgc agtaatctat 20
```

```
<210> SEQ ID NO 556
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin
```

```
<400> SEQUENCE: 556
```

```
ttccagggtcc agggggaaact 20
```

```
<210> SEQ ID NO 557
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin
```

```
<400> SEQUENCE: 557
```

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ccaggcaaga aactttcca 20

<210> SEQ ID NO 558
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 558

ttcagcttct gtaagccagg 20

<210> SEQ ID NO 559
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 559

gacattggca gttgtttcag 20

<210> SEQ ID NO 560
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 560

ggtagcatcc tgtaggacat 20

<210> SEQ ID NO 561
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 561

gagecttcc ttacgggtag 20

<210> SEQ ID NO 562
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 562

cttggagtct tctaggagcc 20

<210> SEQ ID NO 563
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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```
<400> SEQUENCE: 563
cagctcttt actcccttgg                                20

<210> SEQ ID NO 564
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 564
ttgccattgt ttcatcagct                                20

<210> SEQ ID NO 565
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 565
cttacttgcc attgtttcat                                20

<210> SEQ ID NO 566
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 566
cctgacttac ttgccattgt                                20

<210> SEQ ID NO 567
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 567
aaatgcctga cttacttgcc                                20

<210> SEQ ID NO 568
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
      proprocessed human dystrophin

<400> SEQUENCE: 568
agcggaaatg cctgacttac                                20

<210> SEQ ID NO 569
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

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<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 569

gctaaagcgg aaatgcctga

20

<210> SEQ ID NO 570

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery
of PMO

<400> SEQUENCE: 570

Arg Arg Arg Gln Arg Arg Lys Lys Arg Cys
1 5 10

<210> SEQ ID NO 571

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery
of PMO

<400> SEQUENCE: 571

Arg Arg Arg Arg Arg Arg Arg Arg Arg Phe Phe Cys
1 5 10

<210> SEQ ID NO 572

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery
of PMO

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: 3, 6, 9, 12

<223> OTHER INFORMATION: X = 6-aminohexanoic acid

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: 13

<223> OTHER INFORMATION: X = beta alanine

<400> SEQUENCE: 572

Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 573

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery
of PMO

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: 2, 5, 8, 11, 13

<223> OTHER INFORMATION: X = 6-aminohexanoic acid

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: 14

<223> OTHER INFORMATION: X = beta alanine

<400> SEQUENCE: 573

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Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 574
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery
of PMO
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 1, 4, 7, 10, 13
<223> OTHER INFORMATION: X = 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 14
<223> OTHER INFORMATION: X = beta alanine

<400> SEQUENCE: 574

Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 575
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery
of PMO
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 2, 4, 6, 8, 10, 12
<223> OTHER INFORMATION: X = 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 13
<223> OTHER INFORMATION: X = beta alanine

<400> SEQUENCE: 575

Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 576
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery
of PMO
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 2, 4, 6, 8, 10, 12, 14, 16
<223> OTHER INFORMATION: X = 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 17
<223> OTHER INFORMATION: X = beta alanine

<400> SEQUENCE: 576

Arg Xaa
1 5 10 15

Xaa

<210> SEQ ID NO 577
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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```
<220> FEATURE:  
<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery  
of PMO  
<220> FEATURE:  
<221> NAME/KEY: MOD_RES  
<222> LOCATION: 2, 5, 8, 11, 14, 16  
<223> OTHER INFORMATION: X = 6-aminohexanoic acid  
<220> FEATURE:  
<221> NAME/KEY: MOD_RES  
<222> LOCATION: 17  
<223> OTHER INFORMATION: X = beta alanine
```

<400> SEQUENCE: 577

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa
1 5 10 15

Xaa

```
<210> SEQ ID NO 578  
<211> LENGTH: 14  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery  
of PMO  
<220> FEATURE:  
<221> NAME/KEY: MOD_RES  
<222> LOCATION: 2, 8, 13  
<223> OTHER INFORMATION: X = 6-aminohexanoic acid  
<220> FEATURE:  
<221> NAME/KEY: MOD_RES  
<222> LOCATION: 5, 11, 14  
<223> OTHER INFORMATION: X = beta alanine
```

<400> SEQUENCE: 578

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa Xaa
1 5 10

```
<210> SEQ ID NO 579  
<211> LENGTH: 7  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Peptide Transporter for Intracellular Delivery  
of PMO
```

<400> SEQUENCE: 579

Ala Ser Ser Leu Asn Ile Ala
1 5

```
<210> SEQ ID NO 580  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Cell Penetrating Peptide / Homing Peptide /  
PMO Conjugates  
<220> FEATURE:  
<221> NAME/KEY: MOD_RES  
<222> LOCATION: 8  
<223> OTHER INFORMATION: X = a neutral amino acid C(=O) (CHR)n NH-,  
where n is 2 to 7 and each R is independently H or methyl  
<220> FEATURE:  
<221> NAME/KEY: MOD_RES  
<222> LOCATION: 9  
<223> OTHER INFORMATION: X = Beta alanine
```

<400> SEQUENCE: 580

Ala Ser Ser Leu Asn Ile Ala Xaa Xaa

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1 5

```
<210> SEQ ID NO 581
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cell Penetrating Peptide / Homing Peptide /
    PMO Conjugates
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 2, 8, 13, 22
<223> OTHER INFORMATION: X = a neutral amino acid C(=O) (CHR)n NH-,
    where n is 2 to 7 and each R is independently H or methyl
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 5, 11, 14
<223> OTHER INFORMATION: X = beta alanine

<400> SEQUENCE: 581
```

```
Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Xaa Ala Ser
1 5 10 15
Ser Leu Asn Ile Ala Xaa
20
```

```
<210> SEQ ID NO 582
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cell Penetrating Peptide / Homing Peptide /
    PMO Conjugates
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 8, 10, 16
<223> OTHER INFORMATION: X = a neutral amino acid C(=O) (CHR)n NH-,
    where n is 2 to 7 and each R is independently H or methyl
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 13, 19, 21
<223> OTHER INFORMATION: Xaa = beta alanine
```

```
<400> SEQUENCE: 582
Ala Ser Ser Leu Asn Ile Ala Xaa Arg Xaa Arg Arg Xaa
1 5 10 15
Arg Arg Xaa Arg Xaa
20
```

```
<210> SEQ ID NO 583
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cell Penetrating Peptide / Homing Peptide /
    PMO Conjugates
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 2, 8, 13
<223> OTHER INFORMATION: X = a neutral amino acid C(=O) (CHR)n NH-,
    where n is 2 to 7 and each R is independently H or methyl
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 5, 11, 14
<223> OTHER INFORMATION: X = beta alanine
```

```
<400> SEQUENCE: 583
Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa Xaa
1 5 10
```

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-continued

```
<210> SEQ ID NO 584
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

<400> SEQUENCE: 584

ccactcagag ctcagatctt ctaacttcc 29

```
<210> SEQ ID NO 585
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

<400> SEQUENCE: 585

gggatccagt atacttagag gttcc 25

```
<210> SEQ ID NO 586
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

<400> SEQUENCE: 586

cttccactca gagctcagat cttctaa 27

```
<210> SEQ ID NO 587
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

<400> SEQUENCE: 587

acatcaagga agatggcatt tctagtttgg 30

```
<210> SEQ ID NO 588
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

<400> SEQUENCE: 588

ctccaacatc aaggaagatg gcattttctag 30

```
<210> SEQ ID NO 589
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
    proprocessed human dystrophin
```

<400> SEQUENCE: 589

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ttctgtccaa gccccgttga aatc 24

<210> SEQ ID NO 590
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 590

caccacccat caccctcygt g 21

<210> SEQ ID NO 591
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 591

atcatctcggt tgatatcctc aa 22

<210> SEQ ID NO 592
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 592

acatcaagga agatggcatt tctag 25

<210> SEQ ID NO 593
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 593

accagagtaa cagtctgagt aggagc 26

<210> SEQ ID NO 594
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 594

tcaaggaaga tggcatttct 20

<210> SEQ ID NO 595
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

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<400> SEQUENCE: 595

cctctgtat tttataactt gat

23

<210> SEQ ID NO 596

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 596

atcattttt ctcataccctt ctgct

25

<210> SEQ ID NO 597

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 597

ctcataccctt ctgcttgatg atc

23

<210> SEQ ID NO 598

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 598

tggcatttct agtttgg

17

<210> SEQ ID NO 599

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 599

ccagagcagg tacctccaac atc

23

<210> SEQ ID NO 600

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 600

tgttcagctt ctgttagcca ctga

24

<210> SEQ ID NO 601

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 601

tttgtgtctt tctgagaaac

20

<210> SEQ ID NO 602

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 602

cgcggccatt tctcaacag

19

<210> SEQ ID NO 603

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 603

atctgtcaaa tcgcctgcag

20

<210> SEQ ID NO 604

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 604

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<210> SEQ ID NO 605

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 605

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<210> SEQ ID NO 606

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 606

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<210> SEQ ID NO 607

<211> LENGTH: 26

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 607

ccaatgccat cctggagttc ctgtaa

26

<210> SEQ ID NO 608
<211> LENGTH: 31
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 608

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31

<210> SEQ ID NO 609
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 609

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25

<210> SEQ ID NO 610
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 610

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<210> SEQ ID NO 611
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 611

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<210> SEQ ID NO 612
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 612

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<210> SEQ ID NO 613

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<211> LENGTH: 30
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 613

ccaatgccat cctggagtc ctgtaagata 30

<210> SEQ ID NO 614
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 614

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<210> SEQ ID NO 615
<211> LENGTH: 30
<212> TYPE: DNA
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<210> SEQ ID NO 616
<211> LENGTH: 30
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 616

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<210> SEQ ID NO 617
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 617

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<210> SEQ ID NO 618
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 618

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<210> SEQ ID NO 619
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 619

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<210> SEQ ID NO 620
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 620

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<210> SEQ ID NO 621
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 621

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<210> SEQ ID NO 622
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
proprocessed human dystrophin

<400> SEQUENCE: 622

gctgaattat ttcttccccca gttgcattca 30

<210> SEQ ID NO 623
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 623

ggattgctga attatttctt ccccaagttgc 30

<210> SEQ ID NO 624
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 624

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tttgaggattt gctgaattat ttcttccccca 30

<210> SEQ ID NO 625
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 625

gtacttcata ccaactgattc tgaattcttt 30

<210> SEQ ID NO 626
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 626

tcttgactt catcccaactg attctgaattt 30

<210> SEQ ID NO 627
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 627

tgttcttgta ctccatccca ctgattctga 30

<210> SEQ ID NO 628
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 628

cggttctgaa ggtgttcttg tacttcattcc 30

<210> SEQ ID NO 629
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 629

ctcccggttctt gaaggtgttc ttgtacttca 30

<210> SEQ ID NO 630
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 630
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<210> SEQ ID NO 631
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<210> SEQ ID NO 632
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<210> SEQ ID NO 633
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 633
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<210> SEQ ID NO 634
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 634
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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Antisense sequence to target splice site of
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<400> SEQUENCE: 635
ttcagcttct gtaagccagg caaga 25

<210> SEQ ID NO 636
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 636

ggccaaacct cggcttacct gaaat

25

<210> SEQ ID NO 637
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: arginine-rich peptide transport
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1, 3, 4, 7, 9, 10
<223> OTHER INFORMATION: Xaa = K, R or arginine analog
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 2, 8
<223> OTHER INFORMATION: Xaa = a neutral amino acid C(=O) (CHR)n NH-,
where n is 2 to 7 and each R is independently H or
methyl
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5, 6, 11, 12
<223> OTHER INFORMATION: Xaa = an alpha-amino acid having a neutral
aralkyl side chain

<400> SEQUENCE: 637

Xaa
1 5 10

<210> SEQ ID NO 638
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: arginine-rich peptide transport
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 2, 6, 8, 12
<223> OTHER INFORMATION: Xaa = a neutral amino acid C(=O) (CHR)n NH-,
where n is 2 to 7 and each R is independently H or
methyl

<400> SEQUENCE: 638

Arg Xaa Arg Arg Xaa Arg Xaa Arg Arg Arg Xaa
1 5 10

<210> SEQ ID NO 639
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: arginine-rich peptide transport
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: 3, 5, 9
<223> OTHER INFORMATION: Xaa = a neutral amino acid C(=O) (CHR)n NH-,
where n is 2 to 7 and each R is independently H or
methyl

<400> SEQUENCE: 639

Arg Arg Xaa Arg Xaa Arg Arg Arg Xaa
1 5

<210> SEQ ID NO 640
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 640

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24

<210> SEQ ID NO 641
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 641

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21

<210> SEQ ID NO 642
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 642

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24

<210> SEQ ID NO 643
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 643

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24

<210> SEQ ID NO 644
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 644

caatgctcct gacctctgtg c

21

<210> SEQ ID NO 645
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 645

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22

<210> SEQ ID NO 646
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 646

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gcaatgttat ctgcttcctc caacc 25

<210> SEQ ID NO 647
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 647

gctctttcc aggttcaagt gg 22

<210> SEQ ID NO 648
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 648

cttggacaga acttaccgac tgg 23

<210> SEQ ID NO 649
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 649

gcaggatttg gaacagaggc g 21

<210> SEQ ID NO 650
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 650

catctacatt tgtctgccac tgg 23

<210> SEQ ID NO 651
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR Primer

<400> SEQUENCE: 651

gtttcttcca aagcagcctc tcg 23

It is claimed:

1. A composition for use in producing skipping of exon 44 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 1-20, and capable of forming

with the complementary mRNA sequence in the dystrophin-gene exon 44, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

2. The composition of claim 1, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 8, 11 and 12.

3. The composition of claim 1, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

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4. A composition for use in producing skipping of exon 45 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 21-76 and 612 to 624, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 45, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

5. The composition of claim **4**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 27, 29, 34 and 39.

6. The composition of claim **5**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 29 and 34.

7. The composition of claim **4**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

8. A composition for use in producing skipping of exon 46 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 77-125, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 46, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

9. The composition of claim **8**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 77-105.

10. The composition of claim **9**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 82, 84-87, 90, 96, 98, 99 and 101.

11. The composition of claim **8**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

12. A composition for use in producing skipping of exon 47 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 126-169, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 47, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

13. The composition of claim **12**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 126-149.

14. The composition of claim **13**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 126, 128-130, 132, 144 and 146-149.

15. The composition of claim **12**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

16. A composition for use in producing skipping of exon 48 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 170-224 and 634, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 48, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

17. The composition of claim **16**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 170-201 and 634.

18. The composition of claim **17**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 176, 178, 181-183, 194 and 198-201.

19. The composition of claim **16**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

20. A composition for use in producing skipping of exon 49 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 225-266, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 49, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

21. The composition of claim **20**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 225-248.

22. The composition of claim **21**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 227, 229, 234, 236, 237 and 244-248.

23. The composition of claim **20**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

24. A composition for use in producing skipping of exon 50 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 267-308, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 50, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

25. The composition of claim **24**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 277, 287, 290 and 291.

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26. The composition of claim **25**, wherein the compound contains the sequence consisting of SEQ ID NO: 287.

27. The composition of claim **24**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

28. A composition for use in producing skipping of exon 51 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 309-371, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 51, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

29. The composition of claim **28**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 324, 326 and 327.

30. The composition of claim **29**, wherein the compound contains the sequence consisting of SEQ ID NO: 327.

31. The composition of claim **28**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

32. A composition for use in producing skipping of exon 52 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 372-415, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 52, a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

33. The composition of claim **32**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 372-397.

34. The composition of claim **33**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 379-382, 384, 390 and 392-395.

35. The composition of claim **32**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

36. A composition for use in producing skipping of exon 53 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 416-475 and 625-633, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 53 a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

37. The composition of claim **36**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 428, 429 and 431.

38. The composition of claim **37**, wherein the compound contains a sequence consisting of SEQ ID NO: 429.

39. The composition of claim **36**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

40. A composition for use in producing skipping of exon 54 in the processing of human dystrophin pre-processed mRNA, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 476-519, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 54 a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

41. The composition of claim **40**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 476-499.

42. The composition of claim **41**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 479-482, 484, 489 and 491-493.

43. The composition of claim **40**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

44. A composition for use in producing skipping of exon 55 in the processing of human dystrophin-gene pre-processed mRNA transcript, comprising

a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 520-569 and 635, and capable of forming with the complementary mRNA sequence in the dystrophin-gene exon 55 a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C.

45. The composition of claim **44**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 520-546 and 635.

46. The composition of claim **45**, wherein the compound contains a sequence selected from the group consisting of SEQ ID NOS: 524-528, 537, 539, 540, 542 and 544.

47. The composition of claim **44**, wherein the compound is conjugated to an arginine-rich peptide having a sequence selected from the group consisting of SEQ ID NOS: 570-578.

48. A method of treating muscular dystrophy in a subject, comprising administering to the subject an effective amount of a substantially uncharged antisense compound containing 20-35 morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, comprising a sequence selected from the group consisting SEQ ID NOS: 1 to 569 and 612 to 635, and capable of forming with the complementary mRNA sequence in a dystrophin-gene exon a heteroduplex structure between said compound and mRNA having a Tm of at least 45° C., wherein the exon is selected from the group consisting of exons 44-55.

49. The method of claim **48**, wherein the muscular dystrophy is Duchenne's muscular dystrophy (DMD).

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50. The method of claim **48**, wherein the muscular dystrophy is Becker muscular dystrophy (BMD).

51. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 1-20, and the exon is exon 44.

52. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 21-76 and 612 to 624, and the exon is exon 45.

53. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 77-125, and the exon is exon 46.

54. The method of claim **48**, wherein the sequence selected from the group consisting SEQ ID NOS: 126-169, and the exon is exon 47.

55. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 170-224 and 634, and the exon is exon 48.

56. The method of claim **48**, wherein the sequence selected from the group consisting SEQ ID NOS: 225-266, and the exon is exon 49.

57. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 267-308, and the exon is exon 50.

58. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 309-371, and the exon is exon 51.

59. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 372-415, and the exon is exon 52.

60. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 416-475 and 625-633, and the exon is exon 53.

61. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 476-519, and the exon is exon 54.

62. The method of claim **48**, wherein the sequence is selected from the group consisting SEQ ID NOS: 520-569 and 635, and the exon is exon 55.

63. The method of claim **48**, wherein the sequence comprises SEQ ID NO:287.

64. The method of claim **48**, wherein the compound is conjugated to an arginine-rich peptide.

65. The method of claim **64**, wherein the arginine-rich peptide comprises a sequence selected from the group consisting of SEQ ID NOS: 570-578.

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